

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Method for Producing Multiple Unsaturated
Fatty Acids in Plants

<130> 2002/271

<140> 2002_271

<141> 2002-04-26

<160> 64

<170> PatentIn Vers. 2.0

<210> 1

<211> 1687

<212> DNA

<213> Borago officinalis

<220>

<221> CDS

<222> (42) .. (1388)

<223> D6-desaturase

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 Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn His Asp Lys Pro Gly
 10 15 20

gat cta tgg atc tcg att caa ggg aaa gcc tat gat gtt tcg gat tgg 152
 Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr Asp Val Ser Asp Trp
 25 30 35

gtg aaa gac cat cca ggt ggc agc ttt ccc ttg aag agt ctt gct ggt 200
 Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu Lys Ser Leu Ala Gly
 40 45 50

caa gag gta act gat gca ttt gtt gca ttc cat cct gcc tct aca tgg 248
 Gln Glu Val Thr Asp Ala Phe Val Ala Phe His Pro Ala Ser Thr Trp
 55 60 65

aag aat ctt gat aag ttt ttc act ggg tat tat ctt aaa gat tac tct 296
 Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr Leu Lys Asp Tyr Ser
 70 75 80 85

gtt tct gag gtt tct aaa gat tat agg aag ctt gtg ttt gag ttt tct 344
 Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu Val Phe Glu Phe Ser
 90 95 100

aaa atg ggt ttg tat gac aaa aaa ggt cat att atg ttt gca act ttg 392
 Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile Met Phe Ala Thr Leu

105	110	115	
tgc ttt ata gca atg ctg ttt gct atg agt gtt tat ggg gtt ttg ttt Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val Tyr Gly Val Leu Phe 120 125 130			440
tgt gag ggt gtt ttg gta cat ttg ttt tct ggg tgt ttg atg ggg ttt Cys Glu Gly Val Leu Val His Leu Phe Ser Gly Cys Leu Met Gly Phe 135 140 145			488
ctt tgg att cag agt ggt tgg att gga cat gat gct ggg cat tat atg Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp Ala Gly His Tyr Met 150 155 160 165			536
gta gtg tct gat tca agg ctt aat aag ttt atg ggt att ttt gct gca Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met Gly Ile Phe Ala Ala 170 175 180			584
aat tgt ctt tca gga ata agt att ggt tgg tgg aaa tgg aac cat aat Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp Lys Trp Asn His Asn 185 190 195			632
gca cat cac att gcc tgt aat agc ctt gaa tat gac cct gat tta caa Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr Asp Pro Asp Leu Gln 200 205 210			680
tat ata cca ttc ctt gtt gtg tct tcc aag ttt ttt ggt tca ctc acc Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe Phe Gly Ser Leu Thr 215 220 225			728
tct cat ttc tat gag aaa agg ttg act ttt gac tct tta tca aga ttc Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp Ser Leu Ser Arg Phe 230 235 240 245			776
ttt gta agt tat caa cat tgg aca ttt tac cct att atg tgt gct gct Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro Ile Met Cys Ala Ala 250 255 260			824
agg ctc aat atg tat gta caa tct ctc ata atg ttg ttg acc aag aga Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met Leu Leu Thr Lys Arg 265 270 275			872
aat gtg tcc tat cga gct cat gaa ctc ttg gga tgc cta gtg ttc tcg Asn Val Ser Tyr Arg Ala His Glu Leu Leu Gly Cys Leu Val Phe Ser 280 285 290			920
att tgg tac ccg ttg ctt gtt tct tgt ttg cct aat tgg ggt gaa aga Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro Asn Trp Gly Glu Arg 295 300 305			968
att atg ttt gtt att gca agt ttg tca gtg act gga atg caa caa gtt Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr Gly Met Gln Gln Val 310 315 320 325			1016
cag ttc tcc ttg aac cac ttc tct tca agt gtt tat gtt gga aag cct Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val Tyr Val Gly Lys Pro 330 335 340			1064

aaa ggg aat aat tgg ttt gag aaa caa acg gat ggg aca ctt gac att 1112
 Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp Gly Thr Leu Asp Ile
 345 350 355

tct tgt cct cct tgg atg gat tgg ttt cat ggt gga ttg caa ttc caa 1160
 Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly Gly Leu Gln Phe Gln
 360 365 370

att gag cat cat ttg ttt ccc aag atg cct aga tgc aac ctt agg aaa 1208
 Ile Glu His His Leu Phe Pro Lys Met Pro Arg Cys Asn Leu Arg Lys
 375 380 385

atc tcg ccc tac gtg atc gag tta tgc aag aaa cat aat ttg cct tac 1256
 Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys His Asn Leu Pro Tyr
 390 395 400 405

aat tat gca tct ttc tcc aag gcc aat gaa atg aca ctc aga aca ttg 1304
 Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met Thr Leu Arg Thr Leu
 410 415 420

agg aac aca gca ttg cag gct agg gat ata acc aag ccg ctc ccg aag 1352
 Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr Lys Pro Leu Pro Lys
 425 430 435

aat ttg gta tgg gaa gct ctt cac act cat ggt taa aattaccctt 1398
 Asn Leu Val Trp Glu Ala Leu His Thr His Gly
 440 445

agttcatgta ataatttgag attatgtatc tcctatgttt gtgtcttgtc ttggttctac 1458

ttgttggagt cattgcaact tgtcttttat gggtttattag atgtttttta atatatttta 1518

gaggttttgc tttcatctcc attattgatg aataaggagt tgcattttgt caattgttgt 1578

gctcaatatc tgatattttg gaatgtactt tgtaccactg tgttttcagt tgaagctcat 1638

gtgtacttct atagactttg tttaaattggt tatgaaaaaa aaaaaaaaaa 1687

<210> 2

<211> 448

<212> PRT

<213> Borago officinalis

<400> 2

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His Asp Lys Pro Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr
 20 25 30

Asp Val Ser Asp Trp Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu
 35 40 45

Lys Ser Leu Ala Gly Gln Glu Val Thr Asp Ala Phe Val Ala Phe His
 50 55 60

Pro	Ala	Ser	Thr	Trp	Lys	Asn	Leu	Asp	Lys	Phe	Phe	Thr	Gly	Tyr	Tyr	
65					70					75					80	
Leu	Lys	Asp	Tyr	Ser	Val	Ser	Glu	Val	Ser	Lys	Asp	Tyr	Arg	Lys	Leu	
				85					90					95		
Val	Phe	Glu	Phe	Ser	Lys	Met	Gly	Leu	Tyr	Asp	Lys	Lys	Gly	His	Ile	
			100				105						110			
Met	Phe	Ala	Thr	Leu	Cys	Phe	Ile	Ala	Met	Leu	Phe	Ala	Met	Ser	Val	
		115					120					125				
Tyr	Gly	Val	Leu	Phe	Cys	Glu	Gly	Val	Leu	Val	His	Leu	Phe	Ser	Gly	
	130					135					140					
Cys	Leu	Met	Gly	Phe	Leu	Trp	Ile	Gln	Ser	Gly	Trp	Ile	Gly	His	Asp	
145					150					155					160	
Ala	Gly	His	Tyr	Met	Val	Val	Ser	Asp	Ser	Arg	Leu	Asn	Lys	Phe	Met	
				165				170						175		
Gly	Ile	Phe	Ala	Ala	Asn	Cys	Leu	Ser	Gly	Ile	Ser	Ile	Gly	Trp	Trp	
		180					185						190			
Lys	Trp	Asn	His	Asn	Ala	His	His	Ile	Ala	Cys	Asn	Ser	Leu	Glu	Tyr	
		195					200					205				
Asp	Pro	Asp	Leu	Gln	Tyr	Ile	Pro	Phe	Leu	Val	Val	Ser	Ser	Lys	Phe	
	210					215					220					
Phe	Gly	Ser	Leu	Thr	Ser	His	Phe	Tyr	Glu	Lys	Arg	Leu	Thr	Phe	Asp	
225					230					235					240	
Ser	Leu	Ser	Arg	Phe	Phe	Val	Ser	Tyr	Gln	His	Trp	Thr	Phe	Tyr	Pro	
				245					250					255		
Ile	Met	Cys	Ala	Ala	Arg	Leu	Asn	Met	Tyr	Val	Gln	Ser	Leu	Ile	Met	
			260					265						270		
Leu	Leu	Thr	Lys	Arg	Asn	Val	Ser	Tyr	Arg	Ala	His	Glu	Leu	Leu	Gly	
		275					280					285				
Cys	Leu	Val	Phe	Ser	Ile	Trp	Tyr	Pro	Leu	Leu	Val	Ser	Cys	Leu	Pro	
	290					295					300					
Asn	Trp	Gly	Glu	Arg	Ile	Met	Phe	Val	Ile	Ala	Ser	Leu	Ser	Val	Thr	
305					310					315					320	
Gly	Met	Gln	Gln	Val	Gln	Phe	Ser	Leu	Asn	His	Phe	Ser	Ser	Ser	Val	
				325					330					335		
Tyr	Val	Gly	Lys	Pro	Lys	Gly	Asn	Asn	Trp	Phe	Glu	Lys	Gln	Thr	Asp	
			340				345						350			
Gly	Thr	Leu	Asp	Ile	Ser	Cys	Pro	Pro	Trp	Met	Asp	Trp	Phe	His	Gly	
		355					360					365				

Gly Leu Gln Phe Gln Ile Glu His His Leu Phe Pro Lys Met Pro Arg
 370 375 380

Cys Asn Leu Arg Lys Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys
 385 390 395 400

His Asn Leu Pro Tyr Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met
 405 410 415

Thr Leu Arg Thr Leu Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr
 420 425 430

Lys Pro Leu Pro Lys Asn Leu Val Trp Glu Ala Leu His Thr His Gly
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<210> 3

<211> 1192

<212> DNA

<213> Physcomitrella patens

<220>

<221> CDS

<222> (58) .. (930)

<223> D6-elongase

<400> 3

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atg gag gtc gtg gag aga ttc tac ggt gag ttg gat ggg aag gtc tcg 105
 Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
 1 5 10 15

cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg gat 153
 Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
 20 25 30

acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc atc 201
 Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
 35 40 45

gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt ttg 249
 Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
 50 55 60

tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt ttg 297
 Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
 65 70 75 80

ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc agt 345
 Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
 85 90 95

ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg tac 393
 Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
 100 105 110

tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg att	441
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile	
115 120 125	
ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat acc	489
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr	
130 135 140	
gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc cac	537
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His	
145 150 155 160	
gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct cat	585
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His	
165 170 175	
cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca gga	633
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly	
180 185 190	
gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt cga	681
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg	
195 200 205	
agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac ttg	729
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu	
210 215 220	
aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct tac	777
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr	
225 230 235 240	
tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag att	825
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile	
245 250 255	
ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt tac	873
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr	
260 265 270	
gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct aaa	921
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys	
275 280 285	
act gag tga gctgtatcaa gccatagaaa ctctattatg ttagaacctg	970
Thr Glu	
290	
aagttggtgc tttcttatct ccacttatct tttaagcagc atcagttttg aaatgatgtg	1030
tgggcgtggt ctgcaagtag tcatcaatat aatcggcctg agcacttcag atggattgtt	1090
agaacatgag taaaagcggg tattacgggtg tttattttgt accaaatcac cgcacgggtg	1150
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<210> 4

<211> 290

<212> PRT

<213> *Physcomitrella patens*

<400> 4

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Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
 20 25 30

Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
 35 40 45

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
 50 55 60

Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
 65 70 75 80

Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
 85 90 95

Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
 100 105 110

Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
 115 120 125

Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
 130 135 140

Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
 145 150 155 160

Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
 165 170 175

His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
 180 185 190

Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
 195 200 205

Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu
 210 215 220

Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr
 225 230 235 240

Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
 245 250 255

Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
 260 265 270

Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
 275 280 285

Thr Glu
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<210> 5
 <211> 1054
 <212> DNA
 <213> Thraustochytrium

<220>
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 <222> (43) .. (858)
 <223> D6-elongase

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 Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala Arg Tyr Ala Ser
 5 10 15 20

tgc gcg gcc ttc aag tgg caa gtc acg tac gac gcc aag gac agc ttc 150
 Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala Lys Asp Ser Phe
 25 30 35

gtc ggg ccc ctg gga atc cgg gag ccg ctc ggg ctc ctg gtg ggc tcc 198
 Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu Leu Val Gly Ser
 40 45 50

gtg gtc ctc tac ctg agc ctg ctg gcc gtg gtc tac gcg ctg cgg aac 246
 Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr Ala Leu Arg Asn
 55 60 65

tac ctt ggc ggc ctc atg gcg ctc cgc agc gtg cat aac ctc ggg ctc 294
 Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His Asn Leu Gly Leu
 70 75 80

tgc ctc ttc tgc ggc gcc gtg tgg atc tac acg agc tac ctc atg atc 342
 Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser Tyr Leu Met Ile
 85 90 95 100

cag gat ggg cac ttt cgc agc ctc gag gcg gca acg tgc gag ccg ctc 390
 Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr Cys Glu Pro Leu
 105 110 115

aag cat ccg cac ttc cag ctc atc agc ttg ctc ttt gcg ctg tcc aag 438
 Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe Ala Leu Ser Lys
 120 125 130

atc tgg gag tgg ttc gac acg gtg ctc ctc atc gtc aag ggc aac aag 486
 Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val Lys Gly Asn Lys

135	140	145	
ctc cgc ttc ctg cac gtc ttg cac cac gcc acg acc ttt tgg ctc tac			534
Leu Arg Phe Leu His Val Leu His His Ala Thr Thr Phe Trp Leu Tyr			
150	155	160	
gcc atc gac cac atc ttt ctc tcg tcc atc aag tac ggc gtc gcg gtc			582
Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr Gly Val Ala Val			
165	170	175	180
aat gct ttc atc cac acc gtc atg tac gcg cac tac ttc cgc cca ttc			630
Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr Phe Arg Pro Phe			
	185	190	195
ccg aag ggc ttg cgc ccg ctt att acg cag ttg cag atc gtc cag ttc			678
Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln Ile Val Gln Phe			
	200	205	210
att ttc agc atc ggc atc cat acc gcc att tac tgg cac tac gac tgc			726
Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp His Tyr Asp Cys			
	215	220	225
gag ccg ctc gtg cat acc cac ttt tgg gaa tac gtc acg ccc tac ctt			774
Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val Thr Pro Tyr Leu			
	230	235	240
ttc gtc gtg ccc ttc ctc atc ctc ttt ttc aat ttt tac ctg cag cag			822
Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe Tyr Leu Gln Gln			
245	250	255	260
tac gtc ctc gcg ccc gca aaa acc aag aag gca tag ccacgtaaca			868
Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala			
	265	270	
gtagaccagc agcgccgagg acgcgtgccg cgttatcgcg aagcacgaaa taaagaagat			928
catttgattc aacgaggcta cttgcggcca cgagaaaaaa aaaaaaaaaa aaaaaaaaaa			988
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			1048
ctcgag			1054

<210> 6

<211> 271

<212> PRT

<213> Thraustochytrium

<400> 6

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Lys Asp Ser Phe Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu
35 40 45

Leu Val Gly Ser Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr
 50 55 60

Ala Leu Arg Asn Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His
 65 70 75 80

Asn Leu Gly Leu Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser
 85 90 95

Tyr Leu Met Ile Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr
 100 105 110

Cys Glu Pro Leu Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe
 115 120 125

Ala Leu Ser Lys Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val
 130 135 140

Lys Gly Asn Lys Leu Arg Phe Leu His Val Leu His His Ala Thr Thr
 145 150 155 160

Phe Trp Leu Tyr Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr
 165 170 175

Gly Val Ala Val Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr
 180 185 190

Phe Arg Pro Phe Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln
 195 200 205

Ile Val Gln Phe Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp
 210 215 220

His Tyr Asp Cys Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val
 225 230 235 240

Thr Pro Tyr Leu Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe
 245 250 255

Tyr Leu Gln Gln Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala
 260 265 270

<210> 7

<211> 2040

<212> DNA

<213> *Ceratodon purpureus*

<220>

<221> CDS

<222> (176) .. (1627)

<223> D6-desaturase

<400> 7

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gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag tgt gga tgg 802
Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly Trp

ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac cgt acc gcg	850
Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr Ala	
210 215 220 225	
aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt ggc ttt agt	898
Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe Ser	
230 235 240	
gta tca tgg tgg agg acg aag cac aac att cat cat act gct ccg aat	946
Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro Asn	
245 250 255	
gag tgc gac gaa cag tac aca cct cta gac gaa gac att gat act ctc	994
Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr Leu	
260 265 270	
ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt gag agc aag	1042
Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser Lys	
275 280 285	
aga att ttg cga gtg ctt caa tat cag cac tac atg att ctg cct cta	1090
Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro Leu	
290 295 300 305	
ttg ttc atg gcc cgg tac agt tgg act ttt gga agt ttg ctc ttc aca	1138
Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe Thr	
310 315 320	
ttc aat cct gat ttg agc acg acc aag gga ttg ata gag aag gga aca	1186
Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly Thr	
325 330 335	
gtt gct ttt cac tac gcc tgg ttc agt tgg gct gcg ttc cat att ttg	1234
Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile Leu	
340 345 350	
ccg ggt gtc gct aag cct ctt gcg tgg atg gta gca act gag ctt gtg	1282
Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu Val	
355 360 365	
gcc ggt ttg ttg ttg gga ttc gtg ttt acg ttg agt cac aat gga aag	1330
Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly Lys	
370 375 380 385	
gag gtt tac aat gaa tcg aag gac ttc gtg aga gcc cag gtt att acc	1378
Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile Thr	
390 395 400	
acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc act ggg gga	1426
Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly Gly	
405 410 415	
ctc gac acc cag att gag cat cac ctg ttt cca aca atg ccc agg cac	1474
Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His	
420 425 430	

aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc aag aag cac 1522
 Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys His
 435 440 445

ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct gtc gcg gtt 1570
 Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala Val
 450 455 460 465

gtg aag gcg ctc aag gaa att gct gat gaa gcg tca att cgg ctt cac 1618
 Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu His
 470 475 480

gct cac taa gaaatcgctg aactttgact attcattttt ttgcctggc 1667
 Ala His

tacctcaaat gttcgggagc aggtgcttgg cagtgtgttc aaccggagcg cactgaaaat 1727

gtgcagaatc catttccaga aattaccatt cctagctaaa tcttcttttt accagggtcgg 1787

atatatgaaa cttttttgat gcaacaagta gcattcaatt gaagacattg ttcgagatat 1847

aattcgcagt gtttctattc agcgggcata cgtactagtc catatcggcg gttgccgaga 1907

gtttacatta ttagttggca caacgagtag atctagtgtgta aatttctatt tccgcatgta 1967

atattactct gaatatatac cgttatctat tttcctaaaa aaaaaaaaaa aaaaaaaaaa 2027

aaaaaaaaaa aaa 2040

<210> 8

<211> 483

<212> PRT

<213> Ceratodon purpureus

<400> 8

Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser
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Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr
 20 25 30

Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln
 35 40 45

Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser
 50 55 60

Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile
 65 70 75 80

Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro
 85 90 95

Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val
 100 105 110

Phe	Ala	Thr	Phe	His	Pro	Pro	Ala	Ala	Trp	Lys	Gln	Leu	Asn	Asp	Tyr	115	120	125
Tyr	Ile	Gly	Asp	Leu	Ala	Arg	Glu	Glu	Pro	Leu	Asp	Glu	Leu	Leu	Lys	130	135	140
Asp	Tyr	Arg	Asp	Met	Arg	Ala	Glu	Phe	Val	Arg	Glu	Gly	Leu	Phe	Lys	145	150	155
Ser	Ser	Lys	Ala	Trp	Phe	Leu	Leu	Gln	Thr	Leu	Ile	Asn	Ala	Ala	Leu	165	170	175
Phe	Ala	Ala	Ser	Ile	Ala	Thr	Ile	Cys	Tyr	Asp	Lys	Ser	Tyr	Trp	Ala	180	185	190
Ile	Val	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	Val	Gln	Gln	Cys	Gly	195	200	205
Trp	Leu	Ala	His	Asp	Phe	Leu	His	Gln	Gln	Val	Phe	Glu	Asn	Arg	Thr	210	215	220
Ala	Asn	Ser	Phe	Phe	Gly	Tyr	Leu	Phe	Gly	Asn	Cys	Val	Leu	Gly	Phe	225	230	235
Ser	Val	Ser	Trp	Trp	Arg	Thr	Lys	His	Asn	Ile	His	His	Thr	Ala	Pro	245	250	255
Asn	Glu	Cys	Asp	Glu	Gln	Tyr	Thr	Pro	Leu	Asp	Glu	Asp	Ile	Asp	Thr	260	265	270
Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Glu	Ile	Leu	Ala	Thr	Val	Glu	Ser	275	280	285
Lys	Arg	Ile	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	Tyr	Met	Ile	Leu	Pro	290	295	300
Leu	Leu	Phe	Met	Ala	Arg	Tyr	Ser	Trp	Thr	Phe	Gly	Ser	Leu	Leu	Phe	305	310	315
Thr	Phe	Asn	Pro	Asp	Leu	Ser	Thr	Thr	Lys	Gly	Leu	Ile	Glu	Lys	Gly	325	330	335
Thr	Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser	Trp	Ala	Ala	Phe	His	Ile	340	345	350
Leu	Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp	Met	Val	Ala	Thr	Glu	Leu	355	360	365
Val	Ala	Gly	Leu	Leu	Leu	Gly	Phe	Val	Phe	Thr	Leu	Ser	His	Asn	Gly	370	375	380
Lys	Glu	Val	Tyr	Asn	Glu	Ser	Lys	Asp	Phe	Val	Arg	Ala	Gln	Val	Ile	385	390	395
Thr	Thr	Arg	Asn	Thr	Lys	Arg	Gly	Trp	Phe	Asn	Asp	Trp	Phe	Thr	Gly	405	410	415

Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg
 420 425 430
 His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys
 435 440 445
 His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala
 450 455 460
 Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu
 465 470 475 480
 His Ala His

<210> 9

<211> 1467

<212> DNA

<213> Ceratodon purpureus

<220>

<221> CDS

<222> (10) .. (1461)

<223> D6-desaturase

<400> 9

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 Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr
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 tgg agc aag tac agc gtg tac acc cat agc tat gct gga aac tat ggg 99
 Trp Ser Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly
 15 20 25 30
 cct act ttg aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg 147
 Pro Thr Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala
 35 40 45
 gga cag aca ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act 195
 Gly Gln Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr
 50 55 60
 tac tct ctg gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg 243
 Tyr Ser Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp
 65 70 75
 atg atc gtc aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac 291
 Met Ile Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp
 80 85 90
 cac cct gga ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca 339
 His Pro Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr
 95 100 105 110
 gac gtt ttc gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat 387
 Asp Val Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn
 115 120 125

gac tac tac att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg	435
Asp Tyr Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu	
130 135 140	
ctt aaa gac tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt	483
Leu Lys Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu	
145 150 155	
ttc aag agt tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca	531
Phe Lys Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala	
160 165 170	
gct ctc ttt gct gcg agc att gcg act atc tgt tac gac aag agt tac	579
Ala Leu Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr	
175 180 185 190	
tgg gct att gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag	627
Trp Ala Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln	
195 200 205	
tgt gga tgg ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac	675
Cys Gly Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn	
210 215 220	
cgt acc gcg aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt	723
Arg Thr Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu	
225 230 235	
ggc ttt agt gta tca tgg tgg agg acg aag cac aac att cat cat act	771
Gly Phe Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr	
240 245 250	
gct ccg aat gag tgc gac gaa cag tac aca cct cta gac gaa gac att	819
Ala Pro Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile	
255 260 265 270	
gat act ctc ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt	867
Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val	
275 280 285	
gag agc aag aga att ttg cga gtg ctt caa tat cag cac tac atg att	915
Glu Ser Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile	
290 295 300	
ctg cct cta ttg ttc atg gcc cgg tac agt tgg act ttt gga agt ttg	963
Leu Pro Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu	
305 310 315	
ctc ttc aca ttc aat cct gat ttg agc acg acc aag gga ttg ata gag	1011
Leu Phe Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu	
320 325 330	
aag gga aca gtt gct ttt cac tac gcc tgg ttc agt tgg gct gcg ttc	1059
Lys Gly Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe	
335 340 345 350	

cat att ttg ccg ggt gtc gct aag cct ctt gcg tgg atg gta gca act	1107
His Ile Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr	
355 360 365	
gag ctt gtg gcc ggt ttg ttg ttg gga ttc gtg ttt acg ttg agt cac	1155
Glu Leu Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His	
370 375 380	
aat gga aag gag gtt tac aat gaa tcg aag gac ttc gtg aga gcc cag	1203
Asn Gly Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln	
385 390 395	
gtt att acc acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc	1251
Val Ile Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe	
400 405 410	
act ggg gga ctc gac acc cag att gag cat cac ctg ttt cca aca atg	1299
Thr Gly Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met	
415 420 425 430	
ccc agg cac aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc	1347
Pro Arg His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys	
435 440 445	
aag aag cac ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct	1395
Lys Lys His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser	
450 455 460	
gtc gcg gtt gtg aag gcg ctc aag gaa att gct gat gaa gcg tca att	1443
Val Ala Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile	
465 470 475	
cgg ctt cac gct cac taa gtcgac	1467
Arg Leu His Ala His	
480	

<210> 10

<211> 483

<212> PRT

<213> Ceratodon purpureus

<400> 10

Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser	
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Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr	
20 25 30	
Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln	
35 40 45	
Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser	
50 55 60	
Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile	
65 70 75 80	

Val	Lys	Glu	Lys	Val	Tyr	Asp	Ile	Ser	Arg	Phe	Ala	Asp	Asp	His	Pro	
				85					90					95		
Gly	Gly	Thr	Val	Ile	Ser	Thr	Tyr	Phe	Gly	Arg	Asp	Gly	Thr	Asp	Val	
			100					105					110			
Phe	Ala	Thr	Phe	His	Pro	Pro	Ala	Ala	Trp	Lys	Gln	Leu	Asn	Asp	Tyr	
		115					120					125				
Tyr	Ile	Gly	Asp	Leu	Ala	Arg	Glu	Glu	Pro	Leu	Asp	Glu	Leu	Leu	Lys	
	130					135					140					
Asp	Tyr	Arg	Asp	Met	Arg	Ala	Glu	Phe	Val	Arg	Glu	Gly	Leu	Phe	Lys	
145					150					155					160	
Ser	Ser	Lys	Ala	Trp	Phe	Leu	Leu	Gln	Thr	Leu	Ile	Asn	Ala	Ala	Leu	
			165						170						175	
Phe	Ala	Ala	Ser	Ile	Ala	Thr	Ile	Cys	Tyr	Asp	Lys	Ser	Tyr	Trp	Ala	
			180					185					190			
Ile	Val	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	Val	Gln	Gln	Cys	Gly	
		195					200					205				
Trp	Leu	Ala	His	Asp	Phe	Leu	His	Gln	Gln	Val	Phe	Glu	Asn	Arg	Thr	
	210					215					220					
Ala	Asn	Ser	Phe	Phe	Gly	Tyr	Leu	Phe	Gly	Asn	Cys	Val	Leu	Gly	Phe	
225					230					235					240	
Ser	Val	Ser	Trp	Trp	Arg	Thr	Lys	His	Asn	Ile	His	His	Thr	Ala	Pro	
			245						250					255		
Asn	Glu	Cys	Asp	Glu	Gln	Tyr	Thr	Pro	Leu	Asp	Glu	Asp	Ile	Asp	Thr	
		260						265					270			
Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Glu	Ile	Leu	Ala	Thr	Val	Glu	Ser	
		275					280					285				
Lys	Arg	Ile	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	Tyr	Met	Ile	Leu	Pro	
	290					295					300					
Leu	Leu	Phe	Met	Ala	Arg	Tyr	Ser	Trp	Thr	Phe	Gly	Ser	Leu	Leu	Phe	
305					310					315					320	
Thr	Phe	Asn	Pro	Asp	Leu	Ser	Thr	Thr	Lys	Gly	Leu	Ile	Glu	Lys	Gly	
				325					330					335		
Thr	Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser	Trp	Ala	Ala	Phe	His	Ile	
			340					345					350			
Leu	Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp	Met	Val	Ala	Thr	Glu	Leu	
		355					360					365				
Val	Ala	Gly	Leu	Leu	Leu	Gly	Phe	Val	Phe	Thr	Leu	Ser	His	Asn	Gly	
		370				375					380					

Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile
385 390 395 400

Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly
405 410 415

Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg
420 425 430

His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys
435 440 445

His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala
450 455 460

Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu
465 470 475 480

His Ala His

<210> 11

<211> 2160

<212> DNA

<213> Ceratodon purpureus

<220>

<221> CDS

<222> (159) .. (1721)

<223> D6-desaturase

<400> 11

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ttgtgcatga cgaggtgggt gtaatcttcg ccggcaga atg gtg tcc cag ggc ggc 176
Met Val Ser Gln Gly Gly
1 5

ggt ctc tcg cag ggt tcc att gaa gaa aac att gac gtt gag cac ttg 224
Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn Ile Asp Val Glu His Leu
10 15 20

gca acg atg ccc ctc gtc agt gac ttc cta aat gtc ctg gga acg act 272
Ala Thr Met Pro Leu Val Ser Asp Phe Leu Asn Val Leu Gly Thr Thr
25 30 35

ttg ggc cag tgg agt ctt tcc act aca ttc gct ttc aag agg ctc acg 320
Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe Ala Phe Lys Arg Leu Thr
40 45 50

act aag aaa cac agt tcg gac atc tcg gtg gag gca caa aaa gaa tcg 368
Thr Lys Lys His Ser Ser Asp Ile Ser Val Glu Ala Gln Lys Glu Ser
55 60 65 70

gtt gcg cgg ggg cca gtt gag aat att tct caa tcg gtt gcg cag ccc	416
Val Ala Arg Gly Pro Val Glu Asn Ile Ser Gln Ser Val Ala Gln Pro	
75 80 85	
atc agg cgg agg tgg gtg cag gat aaa aag ccg gtt act tac agc ctg	464
Ile Arg Arg Arg Trp Val Gln Asp Lys Lys Pro Val Thr Tyr Ser Leu	
90 95 100	
aag gat gta gct tcg cac gat atg ccc cag gac tgc tgg att ata atc	512
Lys Asp Val Ala Ser His Asp Met Pro Gln Asp Cys Trp Ile Ile Ile	
105 110 115	
aaa gag aag gtg tat gat gtg agc acc ttc gct gag cag cac cct gga	560
Lys Glu Lys Val Tyr Asp Val Ser Thr Phe Ala Glu Gln His Pro Gly	
120 125 130	
ggc acg gtt atc aac acc tac ttc gga cga gac gcc aca gat gtt ttc	608
Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg Asp Ala Thr Asp Val Phe	
135 140 145 150	
tct act ttc cac gca tcc acc tca tgg aag att ctt cag aat ttc tac	656
Ser Thr Phe His Ala Ser Thr Ser Trp Lys Ile Leu Gln Asn Phe Tyr	
155 160 165	
atc ggg aac ctt gtt agg gag gag ccg act ttg gag ctg ctg aag gag	704
Ile Gly Asn Leu Val Arg Glu Glu Pro Thr Leu Glu Leu Leu Lys Glu	
170 175 180	
tac aga gag ttg aga gcc ctt ttc ttg aga gaa cag ctt ttc aag agt	752
Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser	
185 190 195	
tcc aaa tcc tac tac ctt ttc aag act ctc ata aat gtt tcc att gtt	800
Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu Ile Asn Val Ser Ile Val	
200 205 210	
gcc aca agc att gcg ata atc agt ctg tac aag tct tac cgg gcg gtt	848
Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr Lys Ser Tyr Arg Ala Val	
215 220 225 230	
ctg tta tca gcc agt ttg atg ggc ttg ttt att caa cag tgc gga tgg	896
Leu Leu Ser Ala Ser Leu Met Gly Leu Phe Ile Gln Gln Cys Gly Trp	
235 240 245	
ttg tct cac gat ttt cta cac cat cag gta ttt gag aca cgc tgg ctc	944
Leu Ser His Asp Phe Leu His His Gln Val Phe Glu Thr Arg Trp Leu	
250 255 260	
aat gac gtt gtt ggc tat gtg gtc ggc aac gtt gtt ctg gga ttc agt	992
Asn Asp Val Val Gly Tyr Val Val Gly Asn Val Val Leu Gly Phe Ser	
265 270 275	
gtc tcg tgg tgg aag acc aag cac aac ctg cat cat gct gct ccg aat	1040
Val Ser Trp Trp Lys Thr Lys His Asn Leu His His Ala Ala Pro Asn	
280 285 290	
gaa tgc gac caa aag tac aca ccg att gat gag gat att gat act ctc	1088

Glu 295	Cys	Asp	Gln	Lys	Tyr 300	Thr	Pro	Ile	Asp	Glu	Asp	Ile	Asp	Thr	Leu 310		
ccc Pro	atc Ile	att Ile	gct Ala	tgg Trp	agt Ser	aaa Lys	gat Asp	ctc Leu	ttg Leu	gcc Ala	act Thr	gtt Val	gag Glu	agc Ser	aag Lys	1136	
acc Thr	atg Met	ttg Leu	cga Arg	gtt Val	ctt Leu	cag Gln	tac Tyr	cag Gln	cac His	cta Leu	ttc Phe	ttt Phe	ttg Leu	gtt Val	ctt Leu	1184	
ttg Leu	acg Thr	ttt Phe	gcc Ala	cgg Arg	gcg Ala	agt Ser	tgg Trp	cta Leu	ttt Phe	tgg Trp	agc Ser	gcg Ala	gcc Ala	ttc Phe	act Thr	1232	
ctc Leu	agg Arg	ccc Pro	gag Glu	ttg Leu	acc Thr	ctt Leu	ggc Gly	gag Glu	aag Lys	ctt Leu	ttg Leu	gag Glu	agg Arg	gga Gly	acg Thr	1280	
atg Met 375	gct Ala	ttg Leu	cac His	tac Tyr	att Ile	tgg Trp	ttt Phe	aat Asn	agt Ser	gtt Val	gcg Ala	ttt Phe	tat Tyr	ctg Leu	ctc Leu 390	1328	
ccc Pro	gga Gly	tgg Trp	aaa Lys	cca Pro	gtt Val	gta Val	tgg Trp	atg Met	gtg Val	gtc Val	agc Ser	gag Glu	ctc Leu	atg Met	tct Ser	1376	
ggc Gly	ttc Phe	ctg Leu	ctg Leu	gga Gly	tac Tyr	gta Val	ttt Phe	gta Val	ctc Leu	agt Ser	cac His	aat Asn	gga Gly	atg Met	gag Glu	1424	
gtg Val	tac Tyr	aat Asn	acg Thr	tca Ser	aag Lys	gac Asp	ttc Phe	gtg Val	aat Asn	gcc Ala	cag Gln	att Ile	gca Ala	tcg Ser	act Thr	1472	
cgc Arg	gac Asp	atc Ile	aaa Lys	gca Ala	ggg Gly	gtg Val	ttt Phe	aat Asn	gat Asp	tgg Trp	ttc Phe	acc Thr	gga Gly	ggc Gly	ctc Leu	1520	
aac Asn 455	aga Arg	cag Gln	att Ile	gag Glu	cat His	cat His	cta Leu	ttt Phe	cca Pro	acg Thr	atg Met	ccc Pro	agg Arg	cac His	aac Asn 470	1568	
ctt Leu	aat Asn	aaa Lys	att Ile	tct Ser	cct Pro	cac His	gtg Val	gag Glu	act Thr	ttg Leu	tgc Cys	aag Lys	aag Lys	cat His	gga Gly	1616	
ctg Leu	gtc Val	tac Tyr	gaa Glu	gac Asp	gtg Val	agc Ser	atg Met	gct Ala	tcg Ser	ggc Gly	act Thr	tac Tyr	cgg Arg	gtt Val	ttg Leu	1664	
aaa Lys	aca Thr	ctt Leu	aag Lys	gac Asp	gtt Val	gcc Ala	gat Asp	gct Ala	gct Ala	tca Ser	cac His	cag Gln	cag Gln	ctt Leu	gct Ala	1712	
gcg Ala	agt Ser	tga	ggc	atc	gcg	cag	cact	cg	tcga	aac	att	ttt	tg	tct	gtt	atag	1761

520

tgttcatatg tgatcgaggg gaaaaggtcc catgctctga tctattcttc ttagaccaat 1821
 atttttcaat tgaaaggagg ttcctcactt atcttccatc tatcgttgca catcctgcat 1881
 cagagtttagc gttggagtaa tgtaagcac ttgtagatta tgcccacat tgccacattt 1941
 ctgttcgggtt acaatcgttt gattccatgc taccctccgt gttcatctcg ttgttataag 2001
 caagcttgaa aaaacatgct acgagattgg cagacgttgt cttggcagct gtagaggttg 2061
 gttccattca ttgtgtagta cagaactctc tcgtccctgt ttctctacat tacttgttac 2121
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<210> 12

<211> 520

<212> PRT

<213> *Ceratodon purpureus*

<400> 12

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Ile	Asp	Val	Glu	His	Leu	Ala	Thr	Met	Pro	Leu	Val	Ser	Asp	Phe	Leu
			20					25					30		
Asn	Val	Leu	Gly	Thr	Thr	Leu	Gly	Gln	Trp	Ser	Leu	Ser	Thr	Thr	Phe
		35					40					45			
Ala	Phe	Lys	Arg	Leu	Thr	Thr	Lys	Lys	His	Ser	Ser	Asp	Ile	Ser	Val
	50					55					60				
Glu	Ala	Gln	Lys	Glu	Ser	Val	Ala	Arg	Gly	Pro	Val	Glu	Asn	Ile	Ser
65					70					75					80
Gln	Ser	Val	Ala	Gln	Pro	Ile	Arg	Arg	Arg	Trp	Val	Gln	Asp	Lys	Lys
				85					90					95	
Pro	Val	Thr	Tyr	Ser	Leu	Lys	Asp	Val	Ala	Ser	His	Asp	Met	Pro	Gln
			100					105					110		
Asp	Cys	Trp	Ile	Ile	Ile	Lys	Glu	Lys	Val	Tyr	Asp	Val	Ser	Thr	Phe
	115						120					125			
Ala	Glu	Gln	His	Pro	Gly	Gly	Thr	Val	Ile	Asn	Thr	Tyr	Phe	Gly	Arg
	130					135					140				
Asp	Ala	Thr	Asp	Val	Phe	Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys
145					150					155					160
Ile	Leu	Gln	Asn	Phe	Tyr	Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr
			165						170					175	
Leu	Glu	Leu	Leu	Lys	Glu	Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg

180						185						190					
Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu		
195						200						205					
Ile	Asn	Val	Ser	Ile	Val	Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr		
210						215						220					
Lys	Ser	Tyr	Arg	Ala	Val	Leu	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe		
225						230						235					
Ile	Gln	Gln	Cys	Gly	Trp	Leu	Ser	His	Asp	Phe	Leu	His	His	Gln	Val		
245						250						255					
Phe	Glu	Thr	Arg	Trp	Leu	Asn	Asp	Val	Val	Gly	Tyr	Val	Val	Gly	Asn		
260						265						270					
Val	Val	Leu	Gly	Phe	Ser	Val	Ser	Trp	Trp	Lys	Thr	Lys	His	Asn	Leu		
275						280						285					
His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile	Asp		
290						295						300					
Glu	Asp	Ile	Asp	Thr	Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu	Leu		
305						310						315					
Ala	Thr	Val	Glu	Ser	Lys	Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His		
325						330						335					
Leu	Phe	Phe	Leu	Val	Leu	Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu	Phe		
340						345						350					
Trp	Ser	Ala	Ala	Phe	Thr	Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu	Lys		
355						360						365					
Leu	Leu	Glu	Arg	Gly	Thr	Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn	Ser		
370						375						380					
Val	Ala	Phe	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro	Val	Val	Trp	Met	Val		
385						390						395					
Val	Ser	Glu	Leu	Met	Ser	Gly	Phe	Leu	Leu	Gly	Tyr	Val	Phe	Val	Leu		
405						410						415					
Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Thr	Ser	Lys	Asp	Phe	Val	Asn		
420						425						430					
Ala	Gln	Ile	Ala	Ser	Thr	Arg	Asp	Ile	Lys	Ala	Gly	Val	Phe	Asn	Asp		
435						440						445					
Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu	His	His	Leu	Phe	Pro		
450						455						460					
Thr	Met	Pro	Arg	His	Asn	Leu	Asn	Lys	Ile	Ser	Pro	His	Val	Glu	Thr		
465						470						475					
Leu	Cys	Lys	Lys	His	Gly	Leu	Val	Tyr	Glu	Asp	Val	Ser	Met	Ala	Ser		

485

490

495

Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala
 500 505 510

Ser His Gln Gln Leu Ala Ala Ser
 515 520

<210> 13

<211> 1434

<212> DNA

<213> *Phaeodactylum tricornutum*

<220>

<221> CDS

<222> (1) .. (1434)

<223> D6-desaturase

<400> 13

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Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala	
1 5 10 15	
cgc aag atc agt tgg cag gaa gtc aag acc cac gcg tct ccg gag gac	96
Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp	
20 25 30	
gcc tgg atc att cac tcc aat aag gtc tac gac gtg tcc aac tgg cac	144
Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His	
35 40 45	
gaa cat ccc gga ggc gcc gtc att ttc acg cac gcc ggt gac gac atg	192
Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met	
50 55 60	
acg gac att ttc gct gcc ttt cac gca ccc gga tcg cag tcg ctc atg	240
Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met	
65 70 75 80	
aag aag ttc tac att ggc gaa ttg ctc ccg gaa acc acc ggc aag gag	288
Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu	
85 90 95	
ccg cag caa atc gcc ttt gaa aag ggc tac cgc gat ctg cgc tcc aaa	336
Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys	
100 105 110	
ctc atc atg atg ggc atg ttc aag tcc aac aag tgg ttc tac gtc tac	384
Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr	
115 120 125	
aag tgc ctc agc aac atg gcc att tgg gcc gcc gcc tgt gct ctc gtc	432
Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val	
130 135 140	
ttt tac tcg gac cgc ttc tgg gta cac ctg gcc agc gcc gtc atg ctg	480

Phe 145	Tyr	Ser	Asp	Arg	Phe 150	Trp	Val	His	Leu	Ala 155	Ser	Ala	Val	Met	Leu 160	
gga Gly	aca Thr	ttc Phe	ttt Phe	cag Gln	cag Gln	tcg Ser	gga Gly	tgg Trp	ttg Leu	gca Ala	cac His	gac Asp	ttt Phe	ctg Leu	cac His	528
				165					170					175		
cac His	cag Gln	gtc Val	ttc Phe	acc Thr	aag Lys	cgc Arg	aag Lys	cac His	ggg Gly	gat Asp	ctc Leu	gga Gly	gga Gly	ctc Leu	ttt Phe	576
			180					185					190			
tgg Trp	ggg Gly	aac Asn	ctc Leu	atg Met	cag Gln	ggg Gly	tac Tyr	tcc Ser	gta Val	cag Gln	tgg Trp	tgg Trp	aaa Lys	aac Asn	aag Lys	624
		195					200					205				
cac His	aac Asn	gga Gly	cac His	cac His	gcc Ala	gtc Val	ccc Pro	aac Asn	ctc Leu	cac His	tgc Cys	tcc Ser	tcc Ser	gca Ala	gtc Val	672
	210					215					220					
gcg Ala	caa Gln	gat Asp	ggg Gly	gac Asp	ccg Pro	gac Asp	atc Ile	gat Asp	acc Thr	atg Met	ccc Pro	ctt Leu	ctc Leu	gcc Ala	tgg Trp	720
225					230					235					240	
tcc Ser	gtc Val	cag Gln	caa Gln	gcc Ala	cag Gln	tct Ser	tac Tyr	cgg Arg	gaa Glu	ctc Leu	caa Gln	gcc Ala	gac Asp	gga Gly	aag Lys	768
				245					250					255		
gat Asp	tcg Ser	ggg Gly	ttg Leu	gtc Val	aag Lys	ttc Phe	atg Met	atc Ile	cgt Arg	aac Asn	caa Gln	tcc Ser	tac Tyr	ttt Phe	tac Tyr	816
			260				265						270			
ttt Phe	ccc Pro	atc Ile	ttg Leu	ttg Leu	ctc Leu	gcc Ala	cgc Arg	ctg Leu	tcg Ser	tgg Trp	ttg Leu	aac Asn	gag Glu	tcc Ser	ttc Phe	864
	275						280					285				
aag Lys	tgc Cys	gcc Ala	ttt Phe	ggg Gly	ctt Leu	gga Gly	gct Ala	gcg Ala	tcg Ser	gag Glu	aac Asn	gct Ala	gct Ala	ctc Leu	gaa Glu	912
	290					295					300					
ctc Leu	aag Lys	gcc Ala	aag Lys	ggg Gly	ctt Leu	cag Gln	tac Tyr	ccc Pro	ctt Leu	ttg Leu	gaa Glu	aag Lys	gct Ala	ggc Gly	atc Ile	960
305					310					315					320	
ctg Leu	ctg Leu	cac His	tac Tyr	gct Ala	tgg Trp	atg Met	ctt Leu	aca Thr	gtt Val	tcg Ser	tcc Ser	ggc Gly	ttt Phe	gga Gly	cgc Arg	1008
				325					330					335		
ttc Phe	tcg Ser	ttc Phe	gcg Ala	tac Tyr	acc Thr	gca Ala	ttt Phe	tac Tyr	ttt Phe	cta Leu	acc Thr	gcg Ala	acc Thr	gcg Ala	tcc Ser	1056
			340				345					350				
tgt Cys	gga Gly	ttc Phe	ttg Leu	ctc Leu	gcc Ala	att Ile	gtc Val	ttt Phe	ggc Gly	ctc Leu	ggc Gly	cac His	aac Asn	ggc Gly	atg Met	1104
		355					360					365				
gcc Ala	acc Thr	tac Tyr	aat Asn	gcc Ala	gac Asp	gcc Ala	cgt Arg	ccg Pro	gac Asp	ttc Phe	tgg Trp	aag Lys	ctc Leu	caa Gln	gtc Val	1152

370	375	380	
acc acg act cgc aac gtc acg ggc gga cac ggt ttc ccc caa gcc ttt			1200
Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe			
385	390	395	400
gtc gac tgg ttc tgt ggt ggc ctc cag tac caa gtc gac cac cac tta			1248
Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu			
405	410		415
ttc ccc agc ctg ccc cga cac aat ctg gcc aag aca cac gca ctg gtc			1296
Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val			
420	425		430
gaa tcg ttc tgc aag gag tgg ggt gtc cag tac cac gaa gcc gac ctt			1344
Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu			
435	440		445
gtg gac ggg acc atg gaa gtc ttg cac cat ttg ggc agc gtg gcc ggc			1392
Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly			
450	455		460
gaa ttc gtc gtg gat ttt gta cgc gat gga ccc gcc atg taa			1434
Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met			
465	470		475

<210> 14

<211> 477

<212> PRT

<213> Phaeodactylum tricornutum

<400> 14

Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala	
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Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp	
20 25 30	
Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His	
35 40 45	
Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met	
50 55 60	
Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met	
65 70 75 80	
Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu	
85 90 95	
Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys	
100 105 110	
Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr	
115 120 125	

Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val
 130 135 140
 Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu
 145 150 155 160
 Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His
 165 170 175
 His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe
 180 185 190
 Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys
 195 200 205
 His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val
 210 215 220
 Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp
 225 230 235 240
 Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys
 245 250 255
 Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr
 260 265 270
 Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe
 275 280 285
 Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu
 290 295 300
 Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile
 305 310 315 320
 Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg
 325 330 335
 Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser
 340 345 350
 Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met
 355 360 365
 Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val
 370 375 380
 Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe
 385 390 395 400
 Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu
 405 410 415
 Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val
 420 425 430

Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu
 435 440 445

Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly
 450 455 460

Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met
 465 470 475

<210> 15

<211> 1563

<212> DNA

<213> *Ceratodon purpureus*

<220>

<221> CDS

<222> (1) .. (1563)

<223> D6-desaturase

<400> 15

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 1 5 10 15

att gac gtt gag cac ttg gca acg atg ccc ctc gtc agt gac ttc cta 96
 Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu
 20 25 30

aat gtc ctg gga acg act ttg ggc cag tgg agt ctt tcc act aca ttc 144
 Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe
 35 40 45

gct ttc aag agg ctc acg act aag aaa cac agt tcg gac atc tcg gtg 192
 Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val
 50 55 60

gag gca caa aaa gaa tcg gtt gcg cgg ggg cca gtt gag aat att tct 240
 Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser
 65 70 75 80

caa tcg gtt gcg cag ccc atc agg cgg agg tgg gtg cag gat aaa aag 288
 Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys
 85 90 95

ccg gtt act tac agc ctg aag gat gta gct tcg cac gat atg ccc cag 336
 Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln
 100 105 110

gac tgc tgg att ata atc aaa gag aag gtg tat gat gtg agc acc ttc 384
 Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe
 115 120 125

gct gag cag cac cct gga ggc acg gtt atc aac acc tac ttc gga cga 432
 Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg
 130 135 140

gac	gcc	aca	gat	gtt	ttc	tct	act	ttc	cac	gca	tcc	acc	tca	tgg	aag	480
Asp	Ala	Thr	Asp	Val	Phe	Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys	
145					150				155						160	
att	ctt	cag	aat	ttc	tac	atc	ggg	aac	ctt	gtt	agg	gag	gag	ccg	act	528
Ile	Leu	Gln	Asn	Phe	Tyr	Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr	
				165				170						175		
ttg	gag	ctg	ctg	aag	gag	tac	aga	gag	ttg	aga	gcc	ctt	ttc	ttg	aga	576
Leu	Glu	Leu	Leu	Lys	Glu	Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg	
			180					185					190			
gaa	cag	ctt	ttc	aag	agt	tcc	aaa	tcc	tac	tac	ctt	ttc	aag	act	ctc	624
Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu	
		195					200					205				
ata	aat	gtt	tcc	att	gtt	gcc	aca	agc	att	gcg	ata	atc	agt	ctg	tac	672
Ile	Asn	Val	Ser	Ile	Val	Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr	
	210					215					220					
aag	tct	tac	cgg	gcg	gtt	ctg	tta	tca	gcc	agt	ttg	atg	ggc	ttg	ttt	720
Lys	Ser	Tyr	Arg	Ala	Val	Leu	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	
225					230				235						240	
att	caa	cag	tgc	gga	tgg	ttg	tct	cac	gat	ttt	cta	cac	cat	cag	gta	768
Ile	Gln	Gln	Cys	Gly	Trp	Leu	Ser	His	Asp	Phe	Leu	His	His	Gln	Val	
			245					250						255		
ttt	gag	aca	cgc	tgg	ctc	aat	gac	gtt	gtt	ggc	tat	gtg	gtc	ggc	aac	816
Phe	Glu	Thr	Arg	Trp	Leu	Asn	Asp	Val	Val	Gly	Tyr	Val	Val	Gly	Asn	
			260					265					270			
gtt	gtt	ctg	gga	ttc	agt	gtc	tcg	tgg	tgg	aag	acc	aag	cac	aac	ctg	864
Val	Val	Leu	Gly	Phe	Ser	Val	Ser	Trp	Trp	Lys	Thr	Lys	His	Asn	Leu	
		275				280						285				
cat	cat	gct	gct	ccg	aat	gaa	tgc	gac	caa	aag	tac	aca	ccg	att	gat	912
His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile	Asp	
		290				295					300					
gag	gat	att	gat	act	ctc	ccc	atc	att	gct	tgg	agt	aaa	gat	ctc	ttg	960
Glu	Asp	Ile	Asp	Thr	Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu	Leu	
305					310				315						320	
gcc	act	gtt	gag	agc	aag	acc	atg	ttg	cga	gtt	ctt	cag	tac	cag	cac	1008
Ala	Thr	Val	Glu	Ser	Lys	Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	
				325					330					335		
cta	ttc	ttt	ttg	gtt	ctt	ttg	acg	ttt	gcc	cgg	gcg	agt	tgg	cta	ttt	1056
Leu	Phe	Phe	Leu	Val	Leu	Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu	Phe	
			340					345					350			
tgg	agc	gcg	gcc	ttc	act	ctc	agg	ccc	gag	ttg	acc	ctt	ggc	gag	aag	1104
Trp	Ser	Ala	Ala	Phe	Thr	Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu	Lys	
		355				360						365				
ctt	ttg	gag	agg	gga	acg	atg	gct	ttg	cac	tac	att	tgg	ttt	aat	agt	1152

Leu	Leu	Glu	Arg	Gly	Thr	Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn	Ser		
370						375					380						
gtt	gcg	ttt	tat	ctg	ctc	ccc	gga	tgg	aaa	cca	gtt	gta	tgg	atg	gtg	1200	
Val	Ala	Phe	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro	Val	Val	Trp	Met	Val		
385					390				395						400		
gtc	agc	gag	ctc	atg	tct	ggg	ttc	ctg	ctg	gga	tac	gta	ttt	gta	ctc	1248	
Val	Ser	Glu	Leu	Met	Ser	Gly	Phe	Leu	Leu	Gly	Tyr	Val	Phe	Val	Leu		
				405				410						415			
agt	cac	aat	gga	atg	gag	gtg	tac	aat	acg	tca	aag	gac	ttc	gtg	aat	1296	
Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Thr	Ser	Lys	Asp	Phe	Val	Asn		
			420					425					430				
gcc	cag	att	gca	tcg	act	cgc	gac	atc	aaa	gca	ggg	gtg	ttt	aat	gat	1344	
Ala	Gln	Ile	Ala	Ser	Thr	Arg	Asp	Ile	Lys	Ala	Gly	Val	Phe	Asn	Asp		
			435				440					445					
tgg	ttc	acc	gga	ggg	ctc	aac	aga	cag	att	gag	cat	cat	cta	ttt	cca	1392	
Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu	His	His	Leu	Phe	Pro		
	450					455					460						
acg	atg	ccc	agg	cac	aac	ctt	aat	aaa	att	tct	cct	cac	gtg	gag	act	1440	
Thr	Met	Pro	Arg	His	Asn	Leu	Asn	Lys	Ile	Ser	Pro	His	Val	Glu	Thr		
465					470				475						480		
ttg	tgc	aag	aag	cat	gga	ctg	gtc	tac	gaa	gac	gtg	agc	atg	gct	tcg	1488	
Leu	Cys	Lys	Lys	His	Gly	Leu	Val	Tyr	Glu	Asp	Val	Ser	Met	Ala	Ser		
				485				490						495			
ggc	act	tac	cgg	gtt	ttg	aaa	aca	ctt	aag	gac	gtt	gcc	gat	gct	gct	1536	
Gly	Thr	Tyr	Arg	Val	Leu	Lys	Thr	Leu	Lys	Asp	Val	Ala	Asp	Ala	Ala		
			500					505					510				
tca	cac	cag	cag	ctt	gct	gcg	agt	tga								1563	
Ser	His	Gln	Gln	Leu	Ala	Ala	Ser										
		515				520											

<210> 16

<211> 520

<212> PRT

<213> Ceratodon purpureus

<400> 16

Met	Val	Ser	Gln	Gly	Gly	Gly	Leu	Ser	Gln	Gly	Ser	Ile	Glu	Glu	Asn		
1				5					10					15			
Ile	Asp	Val	Glu	His	Leu	Ala	Thr	Met	Pro	Leu	Val	Ser	Asp	Phe	Leu		
			20					25					30				
Asn	Val	Leu	Gly	Thr	Thr	Leu	Gly	Gln	Trp	Ser	Leu	Ser	Thr	Thr	Phe		
		35					40					45					
Ala	Phe	Lys	Arg	Leu	Thr	Thr	Lys	Lys	His	Ser	Ser	Asp	Ile	Ser	Val		
	50						55				60						

Glu	Ala	Gln	Lys	Glu	Ser	Val	Ala	Arg	Gly	Pro	Val	Glu	Asn	Ile	Ser		
65					70					75					80		
Gln	Ser	Val	Ala	Gln	Pro	Ile	Arg	Arg	Arg	Trp	Val	Gln	Asp	Lys	Lys		
				85					90					95			
Pro	Val	Thr	Tyr	Ser	Leu	Lys	Asp	Val	Ala	Ser	His	Asp	Met	Pro	Gln		
			100					105					110				
Asp	Cys	Trp	Ile	Ile	Ile	Lys	Glu	Lys	Val	Tyr	Asp	Val	Ser	Thr	Phe		
		115					120					125					
Ala	Glu	Gln	His	Pro	Gly	Gly	Thr	Val	Ile	Asn	Thr	Tyr	Phe	Gly	Arg		
		130				135					140						
Asp	Ala	Thr	Asp	Val	Phe	Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys		
145					150					155					160		
Ile	Leu	Gln	Asn	Phe	Tyr	Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr		
			165					170						175			
Leu	Glu	Leu	Leu	Lys	Glu	Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg		
			180					185					190				
Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu		
		195					200					205					
Ile	Asn	Val	Ser	Ile	Val	Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr		
	210					215				220							
Lys	Ser	Tyr	Arg	Ala	Val	Leu	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe		
225					230				235					240			
Ile	Gln	Gln	Cys	Gly	Trp	Leu	Ser	His	Asp	Phe	Leu	His	His	Gln	Val		
			245					250						255			
Phe	Glu	Thr	Arg	Trp	Leu	Asn	Asp	Val	Val	Gly	Tyr	Val	Val	Gly	Asn		
			260					265					270				
Val	Val	Leu	Gly	Phe	Ser	Val	Ser	Trp	Trp	Lys	Thr	Lys	His	Asn	Leu		
		275					280					285					
His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile	Asp		
	290					295					300						
Glu	Asp	Ile	Asp	Thr	Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu	Leu		
305					310					315				320			
Ala	Thr	Val	Glu	Ser	Lys	Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His		
				325					330					335			
Leu	Phe	Phe	Leu	Val	Leu	Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu	Phe		
			340					345					350				
Trp	Ser	Ala	Ala	Phe	Thr	Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu	Lys		
		355					360						365				

Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser
 370 375 380

Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val
 385 390 395 400

Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu
 405 410 415

Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn
 420 425 430

Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp
 435 440 445

Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro
 450 455 460

Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr
 465 470 475 480

Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser
 485 490 495

Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala
 500 505 510

Ser His Gln Gln Leu Ala Ala Ser
 515 520

<210> 17

<211> 1578

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> CDS

<222> (1) .. (1578)

<223> D6-desaturase

<400> 17

atg gta ttc gcg ggc ggt gga ctt cag cag ggc tct ctc gaa gaa aac 48
 Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
 1 5 10 15

atc gac gtc gag cac att gcc agt atg tct ctc ttc agc gac ttc ttc 96
 Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
 20 25 30

agt tat gtg tct tca act gtt ggt tcg tgg agc gta cac agt ata caa 144
 Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
 35 40 45

cct ttg aag cgc ctg acg agt aag aag cgt gtt tcg gaa agc gct gcc 192
 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala

50	55	60	
gtg caa tgt ata tca gct gaa gtt cag aga aat tcg agt acc cag gga			240
Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly			
65	70	75	80
act gcg gag gca ctc gca gaa tca gtc gtg aag ccc acg aga cga agg			288
Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg			
	85	90	95
tca tct cag tgg aag aag tcg aca cac ccc cta tca gaa gta gca gta			336
Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val			
	100	105	110
cac aac aag cca agc gat tgc tgg att gtt gta aaa aac aag gtg tat			384
His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr			
	115	120	125
gat gtt tcc aat ttt gcg gac gag cat ccc gga gga tca gtt att agt			432
Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser			
	130	135	140
act tat ttt gga cga gac ggc aca gat gtt ttc tct agt ttt cat gca			480
Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala			
145	150	155	160
gct tct aca tgg aaa att ctt caa gac ttt tac att ggt gac gtg gag			528
Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu			
	165	170	175
agg gtg gag ccg act cca gag ctg ctg aaa gat ttc cga gaa atg aga			576
Arg Val Glu Pro Thr Pro Glu Leu Lys Asp Phe Arg Glu Met Arg			
	180	185	190
gct ctt ttc ctg agg gag caa ctt ttc aaa agt tcg aaa ttg tac tat			624
Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr			
	195	200	205
gtt atg aag ctg ctc acg aat gtt gct att ttt gct gcg agc att gca			672
Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala			
	210	215	220
ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt			720
Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys			
225	230	235	240
atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt			768
Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe			
	245	250	255
ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg			816
Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly			
	260	265	270
tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag			864
Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys			
	275	280	285

gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act	912
Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr	
290 295 300	
tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg	960
Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp	
305 310 315 320	
agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc	1008
Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile	
325 330 335	
ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt	1056
Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg	
340 345 350	
ggc agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc	1104
Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu	
355 360 365	
tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac	1152
Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr	
370 375 380	
ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca	1200
Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro	
385 390 395 400	
tta gta tgg atg gcg gtg act gag ctc atg tcc ggc atg ctg ctg ggc	1248
Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly	
405 410 415	
ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tcg tct	1296
Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser	
420 425 430	
aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga	1344
Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly	
435 440 445	
aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag	1392
Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu	
450 455 460	
cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca	1440
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala	
465 470 475 480	
cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac	1488
Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp	
485 490 495	
gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa	1536
Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu	
500 505 510	

gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa
 Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser
 515 520 525

1578

<210> 18

<211> 525

<212> PRT

<213> *Physcomitrella patens*

<400> 18

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
 1 5 10 15

Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
 20 25 30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
 35 40 45

Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
 50 55 60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
 65 70 75 80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
 85 90 95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
 100 105 110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
 115 120 125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
 130 135 140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
 145 150 155 160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
 165 170 175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
 180 185 190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
 195 200 205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
 210 215 220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
 225 230 235 240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe

245										250					255				
Leu	His	Asn	Gln	Val	Phe	Glu	Thr	Arg	Trp	Leu	Asn	Glu	Val	Val	Gly				
			260					265					270						
Tyr	Val	Ile	Gly	Asn	Ala	Val	Leu	Gly	Phe	Ser	Thr	Gly	Trp	Trp	Lys				
		275					280					285							
Glu	Lys	His	Asn	Leu	His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Thr				
	290					295					300								
Tyr	Gln	Pro	Ile	Asp	Glu	Asp	Ile	Asp	Thr	Leu	Pro	Leu	Ile	Ala	Trp				
305					310					315					320				
Ser	Lys	Asp	Ile	Leu	Ala	Thr	Val	Glu	Asn	Lys	Thr	Phe	Leu	Arg	Ile				
				325					330					335					
Leu	Gln	Tyr	Gln	His	Leu	Phe	Phe	Met	Gly	Leu	Leu	Phe	Phe	Ala	Arg				
			340					345					350						
Gly	Ser	Trp	Leu	Phe	Trp	Ser	Trp	Arg	Tyr	Thr	Ser	Thr	Ala	Val	Leu				
		355					360					365							
Ser	Pro	Val	Asp	Arg	Leu	Leu	Glu	Lys	Gly	Thr	Val	Leu	Phe	His	Tyr				
	370					375					380								
Phe	Trp	Phe	Val	Gly	Thr	Ala	Cys	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro				
385					390					395					400				
Leu	Val	Trp	Met	Ala	Val	Thr	Glu	Leu	Met	Ser	Gly	Met	Leu	Leu	Gly				
			405					410					415						
Phe	Val	Phe	Val	Leu	Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Ser	Ser				
			420					425					430						
Lys	Glu	Phe	Val	Ser	Ala	Gln	Ile	Val	Ser	Thr	Arg	Asp	Ile	Lys	Gly				
		435					440					445							
Asn	Ile	Phe	Asn	Asp	Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu				
	450					455					460								
His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	Asn	Lys	Ile	Ala				
465					470						475				480				
Pro	Arg	Val	Glu	Val	Phe	Cys	Lys	Lys	His	Gly	Leu	Val	Tyr	Glu	Asp				
				485				490						495					
Val	Ser	Ile	Ala	Thr	Gly	Thr	Cys	Lys	Val	Leu	Lys	Ala	Leu	Lys	Glu				
			500					505					510						
Val	Ala	Glu	Ala	Ala	Ala	Glu	Gln	His	Ala	Thr	Thr	Ser							
		515					520					525							

<210> 19

<211> 837

<212> DNA

<213> *Phytophthora infestans*

<220>

<221> CDS

<222> (1) .. (837)

<223> D6-elongase

<400> 19

atg tcg act gag cta ctg cag agc tac tac gcg tgg gcc aac gcc acg	48
Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr	
1 5 10 15	
 gag gcc aag ctg ctg gac tgg gtc gac cct gag ggc ggc tgg aag gtg	96
Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val	
20 25 30	
 cat cct atg gca gac tac ccc cta gcc aac ttc tcc agc gtc tac gcc	144
His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala	
35 40 45	
 atc tgc gtc gga tac ttg ctc ttc gta atc ttc ggc acg gcc ctg atg	192
Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met	
50 55 60	
 aaa atg gga gtc ccc gcc atc aag acc agt cca tta cag ttt gtg tac	240
Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr	
65 70 75 80	
 aac ccc atc caa gtc att gcc tgc tct tat atg tgc gtg gag gcc gcc	288
Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala	
85 90 95	
 atc cag gcc tac cgc aac ggc tac acc gcc gcc ccg tgc aac gcc ttt	336
Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe	
100 105 110	
 aag tcc gac gac ccc gtc atg ggc aac gtt ctg tac ctc ttc tat ctc	384
Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu	
115 120 125	
 tcc aag atg ctc gac ctg tgc gac aca gtc ttc att atc cta gga aag	432
Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys	
130 135 140	
 aag tgg aaa cag ctt tcc atc ttg cac gtg tac cac cac ctt acc gtg	480
Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val	
145 150 155 160	
 ctt ttc gtc tac tat gtg acg ttc cgc gcc gct cag gac ggg gac tca	528
Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser	
165 170 175	
 tat gct acc atc gtg ctc aac ggc ttc gtg cac acc atc atg tac act	576
Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr	
180 185 190	
 tac tac ttc gtc agc gcc cac acg cgc aac att tgg tgg aag aag tac	624

Tyr	Tyr	Phe	Val	Ser	Ala	His	Thr	Arg	Asn	Ile	Trp	Trp	Lys	Lys	Tyr		
		195					200					205					
ctc	acg	cgc	att	cag	ctt	atc	cag	ttc	gtg	acc	atg	aac	gtg	cag	ggc	672	
Leu	Thr	Arg	Ile	Gln	Leu	Ile	Gln	Phe	Val	Thr	Met	Asn	Val	Gln	Gly		
	210					215					220						
tac	ctg	acc	tac	tct	cga	cag	tgc	cca	ggc	atg	cct	cct	aag	gtg	ccg	720	
Tyr	Leu	Thr	Tyr	Ser	Arg	Gln	Cys	Pro	Gly	Met	Pro	Pro	Lys	Val	Pro		
225					230					235					240		
ctc	atg	tac	ctt	gtg	tac	gtg	cag	tca	ctc	ttc	tgg	ctc	ttc	atg	aat	768	
Leu	Met	Tyr	Leu	Val	Tyr	Val	Gln	Ser	Leu	Phe	Trp	Leu	Phe	Met	Asn		
				245					250					255			
ttc	tac	att	cgc	gcg	tac	gtg	ttc	ggc	ccc	aag	aaa	ccg	gcc	gtg	gag	816	
Phe	Tyr	Ile	Arg	Ala	Tyr	Val	Phe	Gly	Pro	Lys	Lys	Pro	Ala	Val	Glu		
			260					265					270				
gaa	tcg	aag	aag	aag	ttg	taa										837	
Glu	Ser	Lys	Lys	Lys	Leu												
		275															

<210> 20

<211> 278

<212> PRT

<213> *Phytophthora infestans*

<400> 20

Met	Ser	Thr	Glu	Leu	Leu	Gln	Ser	Tyr	Tyr	Ala	Trp	Ala	Asn	Ala	Thr		
1				5					10					15			
Glu	Ala	Lys	Leu	Leu	Asp	Trp	Val	Asp	Pro	Glu	Gly	Gly	Trp	Lys	Val		
			20					25					30				
His	Pro	Met	Ala	Asp	Tyr	Pro	Leu	Ala	Asn	Phe	Ser	Ser	Val	Tyr	Ala		
		35					40					45					
Ile	Cys	Val	Gly	Tyr	Leu	Leu	Phe	Val	Ile	Phe	Gly	Thr	Ala	Leu	Met		
	50					55					60						
Lys	Met	Gly	Val	Pro	Ala	Ile	Lys	Thr	Ser	Pro	Leu	Gln	Phe	Val	Tyr		
65					70					75					80		
Asn	Pro	Ile	Gln	Val	Ile	Ala	Cys	Ser	Tyr	Met	Cys	Val	Glu	Ala	Ala		
				85					90					95			
Ile	Gln	Ala	Tyr	Arg	Asn	Gly	Tyr	Thr	Ala	Ala	Pro	Cys	Asn	Ala	Phe		
		100					105						110				
Lys	Ser	Asp	Asp	Pro	Val	Met	Gly	Asn	Val	Leu	Tyr	Leu	Phe	Tyr	Leu		
		115					120					125					
Ser	Lys	Met	Leu	Asp	Leu	Cys	Asp	Thr	Val	Phe	Ile	Ile	Leu	Gly	Lys		
		130				135					140						

Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val
 145 150 155 160
 Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser
 165 170 175
 Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr
 180 185 190
 Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr
 195 200 205
 Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly
 210 215 220
 Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro
 225 230 235 240
 Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn
 245 250 255
 Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu
 260 265 270
 Glu Ser Lys Lys Lys Leu
 275

<210> 21
 <211> 1410
 <212> DNA
 <213> *Phaeodactylum tricornutum*

<220>
 <221> CDS
 <222> (1) .. (1410)
 <223> D5-desaturase

<400> 21
 atg gct ccg gat gcg gat aag ctt cga caa cgc cag acg act gcg gta 48
 Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
 1 5 10 15
 gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt 96
 Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
 20 25 30
 ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat 144
 Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
 35 40 45
 gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt 192
 Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
 50 55 60
 ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat 240
 Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His

65	70	75	80	
acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat	288			
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp				
85 90 95				
ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa	336			
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys				
100 105 110				
cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg	384			
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu				
115 120 125				
gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg	432			
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu				
130 135 140				
cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc	480			
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala				
145 150 155 160				
tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc	528			
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala				
165 170 175				
aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc	576			
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly				
180 185 190				
ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa	624			
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln				
195 200 205				
cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat	672			
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp				
210 215 220				
agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat	720			
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp				
225 230 235 240				
cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg	768			
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met				
245 250 255				
ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att	816			
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile				
260 265 270				
ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac	864			
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp				
275 280 285				
aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct	912			
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala				
290 295 300				

gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc 960
 Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
 305 310 315 320

ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg 1008
 Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
 325 330 335

gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc 1056
 Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
 340 345 350

gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa 1104
 Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
 355 360 365

cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt 1152
 Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
 370 375 380

gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa 1200
 Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
 385 390 395 400

cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc 1248
 His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
 405 410 415

ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac 1296
 Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
 420 425 430

tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac 1344
 Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
 435 440 445

gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc 1392
 Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
 450 455 460

ttg acc gga cgg gcg taa 1410
 Leu Thr Gly Arg Ala
 465 470

<210> 22

<211> 469

<212> PRT

<213> *Phaeodactylum tricornutum*

<400> 22

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
 1 5 10 15

Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
 20 25 30

Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
 35 40 45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
 50 55 60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
 65 70 75 80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
 85 90 95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
 100 105 110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
 115 120 125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
 130 135 140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala
 145 150 155 160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala
 165 170 175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly
 180 185 190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln
 195 200 205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp
 210 215 220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp
 225 230 235 240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met
 245 250 255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile
 260 265 270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp
 275 280 285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala
 290 295 300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
 305 310 315 320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
 325 330 335

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
 340 345 350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
 355 360 365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
 370 375 380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
 385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
 405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
 420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
 435 440 445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
 450 455 460

Leu Thr Gly Arg Ala
 465

<210> 23
 <211> 1344
 <212> DNA
 <213> *Caenorhabditis elegans*

<220>
 <221> CDS
 <222> (1) .. (1344)
 <223> D5-desaturase

<400> 23
 atg gta tta cga gag caa gag cat gag cca ttc ttc att aaa att gat 48
 Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp
 1 5 10 15

gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt 96
 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
 20 25 30

ggg agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc 144
 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
 35 40 45

cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa 192
 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
 50 55 60

ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag 240

Leu 65	Lys	Lys	Glu	Cys	Pro 70	Thr	Gln	Glu	Pro	Glu 75	Ile	Pro	Asp	Ile	Lys 80	
gat Asp	gac Asp	cca Pro	atc Ile	aaa Lys	gga Gly	att Ile	gat Asp	gat Asp	gtg Val	aac Asn	atg Met	gga Gly	act Thr	ttc Phe	aat Asn	288
				85					90					95		
att Ile	tct Ser	gag Glu	aaa Lys	cga Arg	tct Ser	gcc Ala	caa Gln	ata Ile	aat Asn	aaa Lys	agt Ser	ttc Phe	act Thr	gat Asp	cta Leu	336
			100					105					110			
cgt Arg	atg Met	cga Arg	gtt Val	cgt Arg	gca Ala	gaa Glu	gga Gly	ctt Leu	atg Met	gat Asp	gga Gly	tct Ser	cct Pro	ttg Leu	ttc Phe	384
		115					120					125				
tac Tyr	att Ile	aga Arg	aaa Lys	att Ile	ctt Leu	gaa Glu	aca Thr	atc Ile	ttc Phe	aca Thr	att Ile	ctt Leu	ttt Phe	gca Ala	ttc Phe	432
	130					135					140					
tac Tyr	ctt Leu	caa Gln	tac Tyr	cac His	aca Thr	tat Tyr	tat Tyr	ctt Leu	cca Pro	tca Ser	gct Ala	att Ile	cta Leu	atg Met	gga Gly	480
	145				150					155					160	
gtt Val	gcg Ala	tgg Trp	caa Gln	caa Gln	ttg Leu	gga Gly	tgg Trp	tta Leu	atc Ile	cat His	gaa Glu	ttc Phe	gca Ala	cat His	cat His	528
			165					170						175		
cag Gln	ttg Leu	ttc Phe	aaa Lys	aac Asn	aga Arg	tac Tyr	tac Tyr	aat Asn	gat Asp	ttg Leu	gcc Ala	agc Ser	tat Tyr	ttc Phe	gtt Val	576
			180					185					190			
gga Gly	aac Asn	ttt Phe	tta Leu	caa Gln	gga Gly	ttc Phe	tca Ser	tct Ser	ggt Gly	ggt Gly	tgg Trp	aaa Lys	gag Glu	cag Gln	cac His	624
		195					200					205				
aat Asn	gtg Val	cat His	cac His	gca Ala	gcc Ala	aca Thr	aat Asn	gtt Val	gtt Val	gga Gly	cga Arg	gac Asp	gga Gly	gat Asp	ctt Leu	672
	210					215					220					
gat Asp	tta Leu	gtc Val	cca Pro	ttc Phe	tat Tyr	gct Ala	aca Thr	gtg Val	gca Ala	gaa Glu	cat His	ctc Leu	aac Asn	aat Asn	tat Tyr	720
	225				230					235					240	
tct Ser	cag Gln	gat Asp	tca Ser	tgg Trp	gtt Val	atg Met	act Thr	cta Leu	ttc Phe	aga Arg	tgg Trp	caa Gln	cat His	gtt Val	cat His	768
				245					250					255		
tgg Trp	aca Thr	ttc Phe	atg Met	tta Leu	cca Pro	ttc Phe	ctc Leu	cgt Arg	ctc Leu	tcg Ser	tgg Trp	ctt Leu	ctt Leu	cag Gln	tca Ser	816
		260						265					270			
atc Ile	att Ile	ttt Phe	gtt Val	agt Ser	cag Gln	atg Met	cca Pro	act Thr	cat His	tat Tyr	tat Tyr	gac Asp	tat Tyr	tac Tyr	aga Arg	864
		275					280					285				
aat Asn	act Thr	gcg Ala	att Ile	tat Tyr	gaa Glu	cag Gln	gtt Val	ggt Gly	ctc Leu	tct Ser	ttg Leu	cac His	tgg Trp	gct Ala	tgg Trp	912

290	295	300	
tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg			960
Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met			
305	310	315	320
ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta			1008
Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val			
	325	330	335
gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac			1056
Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn			
	340	345	350
atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg			1104
Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met			
	355	360	365
aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag			1152
Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln			
	370	375	380
att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act			1200
Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr			
385	390	395	400
gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac			1248
Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr			
	405	410	415
atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc			1296
Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe			
	420	425	430
cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag			1344
Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala			
	435	440	445

<210> 24

<211> 447

<212> PRT

<213> Caenorhabditis elegans

<400> 24

Met	Val	Leu	Arg	Glu	Gln	Glu	His	Glu	Pro	Phe	Phe	Ile	Lys	Ile	Asp
1				5					10					15	

Gly	Lys	Trp	Cys	Gln	Ile	Asp	Asp	Ala	Val	Leu	Arg	Ser	His	Pro	Gly
			20					25					30		

Gly	Ser	Ala	Ile	Thr	Thr	Tyr	Lys	Asn	Met	Asp	Ala	Thr	Thr	Val	Phe
		35					40					45			

His	Thr	Phe	His	Thr	Gly	Ser	Lys	Glu	Ala	Tyr	Gln	Trp	Leu	Thr	Glu
	50					55					60				

Leu	Lys	Lys	Glu	Cys	Pro	Thr	Gln	Glu	Pro	Glu	Ile	Pro	Asp	Ile	Lys	65	70	75	80
Asp	Asp	Pro	Ile	Lys	Gly	Ile	Asp	Asp	Val	Asn	Met	Gly	Thr	Phe	Asn	85	90	95	
Ile	Ser	Glu	Lys	Arg	Ser	Ala	Gln	Ile	Asn	Lys	Ser	Phe	Thr	Asp	Leu	100	105	110	
Arg	Met	Arg	Val	Arg	Ala	Glu	Gly	Leu	Met	Asp	Gly	Ser	Pro	Leu	Phe	115	120	125	
Tyr	Ile	Arg	Lys	Ile	Leu	Glu	Thr	Ile	Phe	Thr	Ile	Leu	Phe	Ala	Phe	130	135	140	
Tyr	Leu	Gln	Tyr	His	Thr	Tyr	Tyr	Leu	Pro	Ser	Ala	Ile	Leu	Met	Gly	145	150	155	160
Val	Ala	Trp	Gln	Gln	Leu	Gly	Trp	Leu	Ile	His	Glu	Phe	Ala	His	His	165	170	175	
Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val	180	185	190	
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His	195	200	205	
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu	210	215	220	
Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr	225	230	235	240
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His	245	250	255	
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser	260	265	270	
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg	275	280	285	
Asn	Thr	Ala	Ile	Tyr	Glu	Gln	Val	Gly	Leu	Ser	Leu	His	Trp	Ala	Trp	290	295	300	
Ser	Leu	Gly	Gln	Leu	Tyr	Phe	Leu	Pro	Asp	Trp	Ser	Thr	Arg	Ile	Met	305	310	315	320
Phe	Phe	Leu	Val	Ser	His	Leu	Val	Gly	Gly	Phe	Leu	Leu	Ser	His	Val	325	330	335	
Val	Thr	Phe	Asn	His	Tyr	Ser	Val	Glu	Lys	Phe	Ala	Leu	Ser	Ser	Asn	340	345	350	
Ile	Met	Ser	Asn	Tyr	Ala	Cys	Leu	Gln	Ile	Met	Thr	Thr	Arg	Asn	Met	355	360	365	

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
 370 375 380
 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
 385 390 395 400
 Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
 405 410 415
 Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
 420 425 430
 Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
 435 440 445

<210> 25
 <211> 954
 <212> DNA
 <213> *Mortierella alpina*

<220>
 <221> CDS
 <222> (1) .. (954)
 <223> D6-elongase

<400> 25
 atg gcc gcc gca atc ttg gac aag gtc aac ttc ggc att gat cag ccc 48
 Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro
 1 5 10 15
 ttc gga atc aag ctc gac acc tac ttt gct cag gcc tat gaa ctc gtc 96
 Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val
 20 25 30
 acc gga aag tcc atc gac tcc ttc gtc ttc cag gag ggc gtc acg cct 144
 Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro
 35 40 45
 ctc tcg acc cag aga gag gtc gcc atg tgg act atc act tac ttc gtc 192
 Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val
 50 55 60
 gtc atc ttt ggt ggt cgc cag atc atg aag agc cag gac gcc ttc aag 240
 Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys
 65 70 75 80
 ctc aag ccc ctc ttc atc ctc cac aac ttc ctc ctg acg atc gcg tcc 288
 Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser
 85 90 95
 gga tcg ctg ttg ctc ctg ttc atc gag aac ctg gtc ccc atc ctc gcc 336
 Gly Ser Leu Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala
 100 105 110
 aga aac gga ctt ttc tac gcc atc tgc gac gac ggt gcc tgg acc cag 384
 Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln

115	120	125	
cgc ctc gag ctc ctc tac tac ctc aac tac ctg gtc aag tac tgg gag			432
Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu			
130	135	140	
ttg gcc gac acc gtc ttt ttg gtc ctc aag aag aag cct ctt gag ttc			480
Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe			
145	150	155	160
ctg cac tac ttc cac cac tcg atg acc atg gtt ctc tgc ttt gtc cag			528
Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln			
	165	170	175
ctt gga gga tac act tca gtg tcc tgg gtc cct att acc ctc aac ttg			576
Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu			
	180	185	190
act gtc cac gtc ttc atg tac tac tac tac atg cgc tcc gct gcc ggt			624
Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly			
	195	200	205
gtt cgc atc tgg tgg aag cag tac ttg acc act ctc cag atc gtc cag			672
Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln			
	210	215	220
ttc gtt ctt gac ctc gga ttc atc tac ttc tgc gcc tac acc tac ttc			720
Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe			
225	230	235	240
gcc ttc acc tac ttc ccc tgg gct ccc aac gtc ggc aag tgc gcc ggt			768
Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly			
	245	250	255
acc gag ggt gct gct ctc ttt ggc tgc gga ctc ctc tcc agc tat ctc			816
Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu			
	260	265	270
ttg ctc ttt atc aac ttc tac cgc att acc tac aat gcc aag gcc aag			864
Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys			
	275	280	285
gca gcc aag gag cgt gga agc aac ttt acc ccc aag act gtc aag tcc			912
Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser			
	290	295	300
ggc gga tcg ccc aag aag ccc tcc aag agc aag cac atc taa			954
Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile			
305	310	315	

<210> 26

<211> 317

<212> PRT

<213> Mortierella alpina

<400> 26

Met	Ala	Ala	Ala	Ile	Leu	Asp	Lys	Val	Asn	Phe	Gly	Ile	Asp	Gln	Pro	1	5	10	15
Phe	Gly	Ile	Lys	Leu	Asp	Thr	Tyr	Phe	Ala	Gln	Ala	Tyr	Glu	Leu	Val	20	25	30	
Thr	Gly	Lys	Ser	Ile	Asp	Ser	Phe	Val	Phe	Gln	Glu	Gly	Val	Thr	Pro	35	40	45	
Leu	Ser	Thr	Gln	Arg	Glu	Val	Ala	Met	Trp	Thr	Ile	Thr	Tyr	Phe	Val	50	55	60	
Val	Ile	Phe	Gly	Gly	Arg	Gln	Ile	Met	Lys	Ser	Gln	Asp	Ala	Phe	Lys	65	70	75	80
Leu	Lys	Pro	Leu	Phe	Ile	Leu	His	Asn	Phe	Leu	Leu	Thr	Ile	Ala	Ser	85	90	95	
Gly	Ser	Leu	Leu	Leu	Leu	Phe	Ile	Glu	Asn	Leu	Val	Pro	Ile	Leu	Ala	100	105	110	
Arg	Asn	Gly	Leu	Phe	Tyr	Ala	Ile	Cys	Asp	Asp	Gly	Ala	Trp	Thr	Gln	115	120	125	
Arg	Leu	Glu	Leu	Leu	Tyr	Tyr	Leu	Asn	Tyr	Leu	Val	Lys	Tyr	Trp	Glu	130	135	140	
Leu	Ala	Asp	Thr	Val	Phe	Leu	Val	Leu	Lys	Lys	Lys	Pro	Leu	Glu	Phe	145	150	155	160
Leu	His	Tyr	Phe	His	His	Ser	Met	Thr	Met	Val	Leu	Cys	Phe	Val	Gln	165	170	175	
Leu	Gly	Gly	Tyr	Thr	Ser	Val	Ser	Trp	Val	Pro	Ile	Thr	Leu	Asn	Leu	180	185	190	
Thr	Val	His	Val	Phe	Met	Tyr	Tyr	Tyr	Tyr	Met	Arg	Ser	Ala	Ala	Gly	195	200	205	
Val	Arg	Ile	Trp	Trp	Lys	Gln	Tyr	Leu	Thr	Thr	Leu	Gln	Ile	Val	Gln	210	215	220	
Phe	Val	Leu	Asp	Leu	Gly	Phe	Ile	Tyr	Phe	Cys	Ala	Tyr	Thr	Tyr	Phe	225	230	235	240
Ala	Phe	Thr	Tyr	Phe	Pro	Trp	Ala	Pro	Asn	Val	Gly	Lys	Cys	Ala	Gly	245	250	255	
Thr	Glu	Gly	Ala	Ala	Leu	Phe	Gly	Cys	Gly	Leu	Leu	Ser	Ser	Tyr	Leu	260	265	270	
Leu	Leu	Phe	Ile	Asn	Phe	Tyr	Arg	Ile	Thr	Tyr	Asn	Ala	Lys	Ala	Lys	275	280	285	
Ala	Ala	Lys	Glu	Arg	Gly	Ser	Asn	Phe	Thr	Pro	Lys	Thr	Val	Lys	Ser	290	295	300	

Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile
 305 310 315

<210> 27
 <211> 1320
 <212> DNA
 <213> Thraustochytrium

<220>
 <221> CDS
 <222> (1)..(1320)
 <223> D5-desaturase

<400> 27
 atg ggc aag ggc agc gag ggc cgc agc gcg gcg cgc gag atg acg gcc 48
 Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala
 1 5 10 15
 gag gcg aac ggc gac aag cgg aaa acg att ctg atc gag ggc gtc ctg 96
 Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu
 20 25 30
 tac gac gcg acg aac ttt aag cac ccg ggc ggt tcg atc atc aac ttc 144
 Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe
 35 40 45
 ttg acc gag ggc gag gcc ggc gtg gac gcg acg cag gcg tac cgc gag 192
 Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu
 50 55 60
 ttt cat cag cgg tcc ggc aag gcc gac aag tac ctc aag tcg ctg ccg 240
 Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro
 65 70 75 80
 aag ctg gat gcg tcc aag gtg gag tcg cgg ttc tcg gcc aaa gag cag 288
 Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln
 85 90 95
 gcg cgg cgc gac gcc atg acg cgc gac tac gcg gcc ttt cgc gag gag 336
 Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu
 100 105 110
 ctc gtc gcc gag ggg tac ttt gac ccg tcg atc ccg cac atg att tac 384
 Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr
 115 120 125
 cgc gtc gtg gag atc gtg gcg ctc ttc gcg ctc tcg ttc tgg ctc atg 432
 Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met
 130 135 140
 tcc aag gcc tcg ccc acc tcg ctc gtg ctg ggc gtg gtg atg aac ggc 480
 Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly
 145 150 155 160
 att gcg cag ggc cgc tgc ggc tgg gtc atg cac gag atg ggc cac ggg 528
 Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly

385

ttc aag cgc cac aac ctc ccg tac tac gac ctg ccc tac acg agc gcg 1248
 Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala
 405 410 415

gtc tcg acc acc ttt gcc aat ctt tat tcc gtc ggc cac tcg gtc ggc 1296
 Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly
 420 425 430

gcc gac acc aag aag cag gac tga 1320
 Ala Asp Thr Lys Lys Gln Asp
 435 440

<210> 28

<211> 439

<212> PRT

<213> Thraustochytrium

<400> 28

Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala
 1 5 10 15

Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu
 20 25 30

Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe
 35 40 45

Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu
 50 55 60

Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro
 65 70 75 80

Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln
 85 90 95

Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu
 100 105 110

Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr
 115 120 125

Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met
 130 135 140

Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly
 145 150 155 160

Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly
 165 170 175

Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe
 180 185 190

Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His

195					200					205					
Ser	Lys	His	His	Ala	Ala	Pro	Asn	Arg	Leu	Glu	His	Asp	Val	Asp	Leu
210						215					220				
Asn	Thr	Leu	Pro	Leu	Val	Ala	Phe	Asn	Glu	Arg	Val	Val	Arg	Lys	Val
225					230					235					240
Lys	Pro	Gly	Ser	Leu	Leu	Ala	Leu	Trp	Leu	Arg	Val	Gln	Ala	Tyr	Leu
				245					250					255	
Phe	Ala	Pro	Val	Ser	Cys	Leu	Leu	Ile	Gly	Leu	Gly	Trp	Thr	Leu	Tyr
			260					265					270		
Leu	His	Pro	Arg	Tyr	Met	Leu	Arg	Thr	Lys	Arg	His	Met	Glu	Phe	Val
		275					280					285			
Trp	Ile	Phe	Ala	Arg	Tyr	Ile	Gly	Trp	Phe	Ser	Leu	Met	Gly	Ala	Leu
	290					295					300				
Gly	Tyr	Ser	Pro	Gly	Thr	Ser	Val	Gly	Met	Tyr	Leu	Cys	Ser	Phe	Gly
305					310					315					320
Leu	Gly	Cys	Ile	Tyr	Ile	Phe	Leu	Gln	Phe	Ala	Val	Ser	His	Thr	His
			325					330						335	
Leu	Pro	Val	Thr	Asn	Pro	Glu	Asp	Gln	Leu	His	Trp	Leu	Glu	Tyr	Ala
			340					345					350		
Ala	Asp	His	Thr	Val	Asn	Ile	Ser	Thr	Lys	Ser	Trp	Leu	Val	Thr	Trp
	355						360					365			
Trp	Met	Ser	Asn	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr
	370					375					380				
Ala	Pro	Gln	Phe	Arg	Phe	Lys	Glu	Ile	Ser	Pro	Arg	Val	Glu	Ala	Leu
385					390					395					400
Phe	Lys	Arg	His	Asn	Leu	Pro	Tyr	Tyr	Asp	Leu	Pro	Tyr	Thr	Ser	Ala
			405						410					415	
Val	Ser	Thr	Thr	Phe	Ala	Asn	Leu	Tyr	Ser	Val	Gly	His	Ser	Val	Gly
			420					425					430		
Ala	Asp	Thr	Lys	Lys	Gln	Asp									
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<210> 29

<211> 957

<212> DNA

<213> Mortierella alpina

<220>

<221> CDS

<222> (1) .. (957)

<223> D6-elongase

<400> 29

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ttt atg gac ctt gcc acc gct atc ggt gtc cgg gcc gcg ccc tat gtc	96
Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val	
20 25 30	
gat cct ctc gag gcc gcg ctg gtg gcc cag gcc gag aag tac atc ccc	144
Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro	
35 40 45	
acg att gtc cat cac acg cgt ggg ttc ctg gtc gcg gtg gag tcg cct	192
Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro	
50 55 60	
ttg gcc cgt gag ctg ccg ttg atg aac ccg ttc cac gtg ctg ttg atc	240
Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile	
65 70 75 80	
gtg ctc gct tat ttg gtc acg gtc ttt gtg ggc atg cag atc atg aag	288
Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys	
85 90 95	
aac ttt gag cgg ttc gag gtc aag acg ttt tcg ctc ctg cac aac ttt	336
Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe	
100 105 110	
tgt ctg gtc tcg atc agc gcc tac atg tgc ggt ggg atc ctg tac gag	384
Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu	
115 120 125	
gct tat cag gcc aac tat gga ctg ttt gag aac gct gct gat cat acc	432
Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr	
130 135 140	
ttc aag ggt ctt cct atg gcc aag atg atc tgg ctc ttc tac ttc tcc	480
Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser	
145 150 155 160	
aag atc atg gag ttt gtc gac acc atg atc atg gtc ctc aag aag aac	528
Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn	
165 170 175	
aac cgc cag atc tcc ttc ttg cac gtt tac cac cac agc tcc atc ttc	576
Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe	
180 185 190	
acc atc tgg tgg ttg gtc acc ttt gtt gca ccc aac ggt gaa gcc tac	624
Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr	
195 200 205	
ttc tct gct gcg ttg aac tcg ttc atc cat gtg atc atg tac ggc tac	672
Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr	
210 215 220	

tac ttc ttg tcg gcc ttg ggc ttc aag cag gtg tcg ttc atc aag ttc 720
 Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe
 225 230 235 240

tac atc acg cgc tcg cag atg aca cag ttc tgc atg atg tcg gtc cag 768
 Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln
 245 250 255

tct tcc tgg gac atg tac gcc atg aag gtc ctt ggc cgc ccc gga tac 816
 Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr
 260 265 270

ccc ttc ttc atc acg gct ctg ctt tgg ttc tac atg tgg acc atg ctc 864
 Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu
 275 280 285

ggc ctc ttc tac aac ttt tac aga aag aac gcc aag ttg gcc aag cag 912
 Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln
 290 295 300

gcc aag gcc gac gct gcc aag gag aag gca agg aag ttg cag taa 957
 Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln
 305 310 315

<210> 30

<211> 318

<212> PRT

<213> Mortierella alpina

<400> 30

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Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val
 20 25 30

Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro
 35 40 45

Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro
 50 55 60

Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile
 65 70 75 80

Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys
 85 90 95

Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe
 100 105 110

Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu
 115 120 125

Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr

130	135	140	
Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser			
145	150	155	160
Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn			
	165	170	175
Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe			
	180	185	190
Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr			
	195	200	205
Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr			
	210	215	220
Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe			
225	230	235	240
Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln			
	245	250	255
Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr			
	260	265	270
Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu			
	275	280	285
Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln			
	290	295	300
Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln			
305	310	315	

<210> 31
 <211> 1374
 <212> DNA
 <213> Mortierella alpina

<220>
 <221> CDS
 <222> (1) .. (1374)
 <223> D6-desaturase

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aat gcc gag gct ctg aat gag ggc aag aag gat gcc gag gca ccc ttc		96
Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe		
20 25 30		
ttg atg atc atc gac aac aag gtg tac gat gtt cgc gag ttc gtc cct		144
Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro		

35	40	45	
gat cat ccc ggt gga agt gtg att ctc acg cac gtt ggc aag gac ggc Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly			192
50	55	60	
act gac gtc ttt gac act ttt cac ccc gag gct gct tgg gag act ctt Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu			240
65	70	75	80
gcc aac ttt tac gtt ggt gat att gac gag agc gac cgc gat atc aag Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys			288
	85	90	95
aat gat gac ttt gcg gcc gag gtc cgc aag ctg cgt acc ttg ttc cag Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln			336
	100	105	110
tct ctt ggt tac tac gat tct tcc aag gca tac tac gcc ttc aag gtc Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val			384
	115	120	125
tcg ttc aac ctc tgc atc tgg ggt ttg tcg acg gtc att gtg gcc aag Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys			432
	130	135	140
tgg ggc cag acc tcg acc ctc gcc aac gtg ctc tcg gct gcg ctt ttg Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu			480
	145	150	155
ggt ctg ttc tgg cag cag tgc gga tgg ttg gct cac gac ttt ttg cat Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His			528
	165	170	175
cac cag gtc ttc cag gac cgt ttc tgg ggt gat ctt ttc ggc gcc ttc His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe			576
	180	185	190
ttg gga ggt gtc tgc cag ggc ttc tcg tcc tcg tgg tgg aag gac aag Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys			624
	195	200	205
cac aac act cac cac gcc gcc ccc aac gtc cac ggc gag gat ccc gac His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp			672
	210	215	220
att gac acc cac cct ctg ttg acc tgg agt gag cat gcg ttg gag atg Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met			720
	225	230	235
ttc tcg gat gtc cca gat gag gag ctg acc cgc atg tgg tcg cgt ttc Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe			768
	245	250	255
atg gtc ctg aac cag acc tgg ttt tac ttc ccc att ctc tcg ttt gcc Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala			816
	260	265	270

cgt ctc tcc tgg tgc ctc cag tcc att ctc ttt gtg ctg cct aac ggt	864
Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly	
275 280 285	
cag gcc cac aag ccc tcg ggc gcg cgt gtg ccc atc tcg ttg gtc gag	912
Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu	
290 295 300	
cag ctg tcg ctt gcg atg cac tgg acc tgg tac ctc gcc acc atg ttc	960
Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe	
305 310 315 320	
ctg ttc atc aag gat ccc gtc aac atg ctg gtg tac ttt ttg gtg tcg	1008
Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser	
325 330 335	
cag gcg gtg tgc gga aac ttg ttg gcg atc gtg ttc tcg ctc aac cac	1056
Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His	
340 345 350	
aac ggt atg cct gtg atc tcg aag gag gag gcg gtc gat atg gat ttc	1104
Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe	
355 360 365	
ttc acg aag cag atc atc acg ggt cgt gat gtc cac ccg ggt cta ttt	1152
Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe	
370 375 380	
gcc aac tgg ttc acg ggt gga ttg aac tat cag atc gag cac cac ttg	1200
Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu	
385 390 395 400	
ttc cct tcg atg cct cgc cac aac ttt tca aag atc cag cct gct gtc	1248
Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val	
405 410 415	
gag acc ctg tgc aaa aag tac aat gtc cga tac cac acc acc ggt atg	1296
Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met	
420 425 430	
atc gag gga act gca gag gtc ttt agc cgt ctg aac gag gtc tcc aag	1344
Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys	
435 440 445	
gct gcc tcc aag atg ggt aag gcg cag taa	1374
Ala Ala Ser Lys Met Gly Lys Ala Gln	
450 455	

<210> 32

<211> 457

<212> PRT

<213> Mortierella alpina

<400> 32

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Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe	20	25	30
Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro	35	40	45
Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly	50	55	60
Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu	65	70	75
Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys	85	90	95
Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln	100	105	110
Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val	115	120	125
Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys	130	135	140
Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu	145	150	155
Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His	165	170	175
His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe	180	185	190
Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys	195	200	205
His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp	210	215	220
Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met	225	230	235
Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe	245	250	255
Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala	260	265	270
Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly	275	280	285
Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu	290	295	300
Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe			

305		310		315		320
Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser	325		330		335	
Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His	340		345		350	
Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe	355		360		365	
Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe	370		375		380	
Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu	385		390		395	400
Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val	405		410		415	
Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met	420		425		430	
Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys	435		440		445	
Ala Ala Ser Lys Met Gly Lys Ala Gln	450		455			

<210> 33

<211> 3598

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant
promoter-terminator expression cassette in vector
pUC19

<400> 33

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accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc 240
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tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt cggcgcgccg agctcctcga 420
gcaaatttac acattgccac taaacgtcta aacccttgta atttggtttt gttttactat 480

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 tttatgctaa cgtttgccaa cacttagcaa tttgcaagtt gattaattga ttctaaatta 600
 tttttgtctt cttaaatacat atactaatca actggaaatg taaatatttg ctaatatctt 660
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 aataaacaaa taggggttcc gcgcacattt ccccgaaaag tgccacctga cgtctaagaa 3540
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<210> 34

<211> 3590

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant
 promoter-terminator expression cassette in vector
 pUC19

<400> 34

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<210> 35
 <211> 3584
 <212> DNA
 <213> Unknown

<220>
 <223> Sequence constitutes a plant
 promoter-terminator expression cassette in vector
 pUC19

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<210> 36

<211> 4507

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant
 promoter-terminator expression cassette in vector
 pUC19

<400> 36

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<210> 37

<211> 5410

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant
 promoter-terminator expression cassette in vector
 pUC19

<400> 37

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<213> Unknown

<220>

<223> Plant expression vector with two
promoter-terminator expression cassettes

<400> 41

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<220>

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Phe Cys Phe Ala Leu Ser Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln	
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gct att acc tgg cgg tac tct ctc tgg ggc aat gca tac aat cct aaa	11908
Ala Ile Thr Trp Arg Tyr Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys	
110 115 120	
cat aaa gag atg gcg att ctg gta tac ttg ttc tac atg tct aag tac	11956
His Lys Glu Met Ala Ile Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr	
125 130 135	
gtg gaa ttc atg gat acc gtt atc atg ata ctg aag cgc agc acc agg	12004
Val Glu Phe Met Asp Thr Val Ile Met Ile Leu Lys Arg Ser Thr Arg	
140 145 150	
caa ata agc ttc ctc cac gtt tat cat cat tct tca att tcc ctc att	12052
Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Ser Leu Ile	
155 160 165 170	
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Trp Trp Ala Ile Ala His His Ala Pro Gly Gly Glu Ala Tyr Trp Ser	
175 180 185	
gcg gct ctg aac tca gga gtg cat gtt ctc atg tat gcg tat tac ttc	12148
Ala Ala Leu Asn Ser Gly Val His Val Leu Met Tyr Ala Tyr Tyr Phe	
190 195 200	
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Leu Ala Ala Cys Leu Arg Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu	
205 210 215	
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Phe Trp Gly Arg Tyr Leu Thr Gln Phe Gln Met Phe Gln Phe Met Leu	
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Asn Leu Val Gln Ala Tyr Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro	
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Gln Trp Leu Ile Lys Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe	
255 260 265	

ctt ttc ggc aat ttt tac gta caa aaa tac atc aaa ccc tct gac gga 12388
 Leu Phe Gly Asn Phe Tyr Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly
 270 275 280

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 Lys Gln Lys Gly Ala Lys Thr Glu
 285 290

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gga ctt cag cag ggc tct ctc gaa gaa aac atc gac gtc gag cac att 13378
 Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile
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 Ala Ser Met Ser Leu Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr
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 Val Gly Ser Trp Ser Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr
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 Ser Lys Lys Arg Val Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala
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gaa gtt cag aga aat tcg agt acc cag gga act gcg gag gca ctc gca 13570

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Glu	Ser	Val	Val	Lys	Pro	Thr	Arg	Arg	Arg	Ser	Ser	Gln	Trp	Lys	Lys		
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Ser	Thr	His	Pro	Leu	Ser	Glu	Val	Ala	Val	His	Asn	Lys	Pro	Ser	Asp		
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tgc	tgg	att	gtt	gta	aaa	aac	aag	gtg	tat	gat	gtt	tcc	aat	ttt	gcg	13714	
Cys	Trp	Ile	Val	Val	Lys	Asn	Lys	Val	Tyr	Asp	Val	Ser	Asn	Phe	Ala		
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caa	ctt	ttc	aaa	agt	tcg	aaa	ttg	tac	tat	gtt	atg	aag	ctg	ctc	acg	13954	
Gln	Leu	Phe	Lys	Ser	Ser	Lys	Leu	Tyr	Tyr	Val	Met	Lys	Leu	Leu	Thr		
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aat	gtt	gct	att	ttt	gct	gcg	agc	att	gca	ata	ata	tgt	tgg	agc	aag	14002	
Asn	Val	Ala	Ile	Phe	Ala	Ala	Ser	Ile	Ala	Ile	Ile	Cys	Trp	Ser	Lys		
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act	att	tca	gcg	gtt	ttg	gct	tca	gct	tgt	atg	atg	gct	ctg	tgt	ttc	14050	
Thr	Ile	Ser	Ala	Val	Leu	Ala	Ser	Ala	Cys	Met	Met	Ala	Leu	Cys	Phe		
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caa	cag	tgc	gga	tgg	cta	tcc	cat	gat	ttt	ctc	cac	aat	cag	gtg	ttt	14098	
Gln	Gln	Cys	Gly	Trp	Leu	Ser	His	Asp	Phe	Leu	His	Asn	Gln	Val	Phe		
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gag	aca	cgc	tgg	ctt	aat	gaa	gtt	gtc	ggg	tat	gtg	atc	ggc	aac	gcc	14146	
Glu	Thr	Arg	Trp	Leu	Asn	Glu	Val	Val	Gly	Tyr	Val	Ile	Gly	Asn	Ala		
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gtt	ctg	ggg	ttt	agt	aca	ggg	tgg	tgg	aag	gag	aag	cat	aac	ctt	cat	14194	
Val	Leu	Gly	Phe	Ser	Thr	Gly	Trp	Trp	Lys	Glu	Lys	His	Asn	Leu	His		
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His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Thr	Tyr	Gln	Pro	Ile	Asp	Glu		

600

gat Asp	att Ile	gat Asp	act Thr	ctc Leu	ccc Pro	ctc Leu	att Ile	gcc Ala	tgg Trp	agc Ser	aag Lys	gac Asp	ata Ile	ctg Leu	gcc Ala	14290
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650			655						660						665	
ttg Leu	gag Glu	aag Lys	gga Gly	act Thr	gtt Val	ctg Leu	ttt Phe	cac His	tac Tyr	ttt Phe	tgg Trp	ttc Phe	gtc Val	ggg Gly	aca Thr	14482
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gcg Ala	tgc Cys	tat Tyr	ctt Leu	ctc Leu	cct Pro	ggt Gly	tgg Trp	aag Lys	cca Pro	tta Leu	gta Val	tgg Trp	atg Met	gcg Ala	gtg Val	14530
			685			690						695				
act Thr	gag Glu	ctc Leu	atg Met	tcc Ser	ggc Gly	atg Met	ctg Leu	ctg Leu	ggc Gly	ttt Phe	gta Val	ttt Phe	gta Val	ctt Leu	agc Ser	14578
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cac His	aat Asn	ggg Gly	atg Met	gag Glu	gtt Val	tat Tyr	aat Asn	tcg Ser	tct Ser	aaa Lys	gaa Glu	ttc Phe	gtg Val	agt Ser	gca Ala	14626
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cag Gln	atc Ile	gta Val	tcc Ser	aca Thr	cgg Arg	gat Asp	atc Ile	aaa Lys	gga Gly	aac Asn	ata Ile	ttc Phe	aac Asn	gac Asp	tgg Trp	14674
730			735						740						745	
ttc Phe	act Thr	ggt Gly	ggc Gly	ctt Leu	aac Asn	agg Arg	caa Gln	ata Ile	gag Glu	cat His	cat His	ctt Leu	ttc Phe	cca Pro	aca Thr	14722
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atg Met	ccc Pro	agg Arg	cat His	aat Asn	tta Leu	aac Asn	aaa Lys	ata Ile	gca Ala	cct Pro	aga Arg	gtg Val	gag Glu	gtg Val	ttc Phe	14770
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tgt Cys	aag Lys	aaa Lys	cac His	ggt Gly	ctg Leu	gtg Val	tac Tyr	gaa Glu	gac Asp	gta Val	tct Ser	att Ile	gct Ala	acc Thr	ggc Gly	14818
			780			785						790				
act Thr	tgc Cys	aag Lys	gtt Val	ttg Leu	aaa Lys	gca Ala	ttg Leu	aag Lys	gaa Glu	gtc Val	gcg Ala	gag Glu	gct Ala	gcg Ala	gca Ala	14866
			795			800						805				
gag Glu	cag Gln	cat His	gct Ala	acc Thr	acc Thr	agt Ser	taa	gctagcgtta			accctgcttt			aatgagatat		14920
810			815													

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Leu	Gln	Ala	Leu	Val	Leu	Val	His	Asn	Leu	Phe	Cys	Phe	Ala	Leu	Ser
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Leu	Tyr	Met	Cys	Val	Gly	Ile	Ala	Tyr	Gln	Ala	Ile	Thr	Trp	Arg	Tyr
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Ser	Leu	Trp	Gly	Asn	Ala	Tyr	Asn	Pro	Lys	His	Lys	Glu	Met	Ala	Ile
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Val	Ile	Met	Ile	Leu	Lys	Arg	Ser	Thr	Arg	Gln	Ile	Ser	Phe	Leu	His
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Val	Tyr	His	His	Ser	Ser	Ile	Ser	Leu	Ile	Trp	Trp	Ala	Ile	Ala	His

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His	Ala	Pro	Gly	Gly	Glu	Ala	Tyr	Trp	Ser	Ala	Ala	Leu	Asn	Ser	Gly				
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Val	His	Val	Leu	Met	Tyr	Ala	Tyr	Tyr	Phe	Leu	Ala	Ala	Cys	Leu	Arg				
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Ser	Ser	Pro	Lys	Leu	Lys	Asn	Lys	Tyr	Leu	Phe	Trp	Gly	Arg	Tyr	Leu				
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Thr	Gln	Phe	Gln	Met	Phe	Gln	Phe	Met	Leu	Asn	Leu	Val	Gln	Ala	Tyr				
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Tyr	Asp	Met	Lys	Thr	Asn	Ala	Pro	Tyr	Pro	Gln	Trp	Leu	Ile	Lys	Ile				
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Leu	Phe	Tyr	Tyr	Met	Ile	Ser	Leu	Leu	Phe	Leu	Phe	Gly	Asn	Phe	Tyr				
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Val	Gln	Lys	Tyr	Ile	Lys	Pro	Ser	Asp	Gly	Lys	Gln	Lys	Gly	Ala	Lys				
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Ser	Tyr	Val	Ser	Ser	Thr	Val	Gly	Ser	Trp	Ser	Val	His	Ser	Ile	Gln				
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Pro	Leu	Lys	Arg	Leu	Thr	Ser	Lys	Lys	Arg	Val	Ser	Glu	Ser	Ala	Ala				
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Val	Gln	Cys	Ile	Ser	Ala	Glu	Val	Gln	Arg	Asn	Ser	Ser	Thr	Gln	Gly				
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Thr	Ala	Glu	Ala	Leu	Ala	Glu	Ser	Val	Val	Lys	Pro	Thr	Arg	Arg	Arg				
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Ser	Ser	Gln	Trp	Lys	Lys	Ser	Thr	His	Pro	Leu	Ser	Glu	Val	Ala	Val				
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His	Asn	Lys	Pro	Ser	Asp	Cys	Trp	Ile	Val	Val	Lys	Asn	Lys	Val	Tyr				
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Asp	Val	Ser	Asn	Phe	Ala	Asp	Glu	His	Pro	Gly	Gly	Ser	Val	Ile	Ser	130	135	140
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Ala	Ser	Thr	Trp	Lys	Ile	Leu	Gln	Asp	Phe	Tyr	Ile	Gly	Asp	Val	Glu	165	170	175
Arg	Val	Glu	Pro	Thr	Pro	Glu	Leu	Leu	Lys	Asp	Phe	Arg	Glu	Met	Arg	180	185	190
Ala	Leu	Phe	Leu	Arg	Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Leu	Tyr	Tyr	195	200	205
Val	Met	Lys	Leu	Leu	Thr	Asn	Val	Ala	Ile	Phe	Ala	Ala	Ser	Ile	Ala	210	215	220
Ile	Ile	Cys	Trp	Ser	Lys	Thr	Ile	Ser	Ala	Val	Leu	Ala	Ser	Ala	Cys	225	230	235
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Leu	His	Asn	Gln	Val	Phe	Glu	Thr	Arg	Trp	Leu	Asn	Glu	Val	Val	Gly	260	265	270
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Glu	Lys	His	Asn	Leu	His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Thr	290	295	300
Tyr	Gln	Pro	Ile	Asp	Glu	Asp	Ile	Asp	Thr	Leu	Pro	Leu	Ile	Ala	Trp	305	310	315
Ser	Lys	Asp	Ile	Leu	Ala	Thr	Val	Glu	Asn	Lys	Thr	Phe	Leu	Arg	Ile	325	330	335
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Gly	Ser	Trp	Leu	Phe	Trp	Ser	Trp	Arg	Tyr	Thr	Ser	Thr	Ala	Val	Leu	355	360	365
Ser	Pro	Val	Asp	Arg	Leu	Leu	Glu	Lys	Gly	Thr	Val	Leu	Phe	His	Tyr	370	375	380
Phe	Trp	Phe	Val	Gly	Thr	Ala	Cys	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro	385	390	395
Leu	Val	Trp	Met	Ala	Val	Thr	Glu	Leu	Met	Ser	Gly	Met	Leu	Leu	Gly	405	410	415
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Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
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 Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
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 Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
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caa ctt ttc aaa agt tcg aaa ttg tac tat gtt atg aag ctg ctc acg	13954
Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr Val Met Lys Leu Leu Thr	
490 495 500 505	
aat gtt gct att ttt gct gcg agc att gca ata ata tgt tgg agc aag	14002
Asn Val Ala Ile Phe Ala Ala Ser Ile Ala Ile Ile Cys Trp Ser Lys	
510 515 520	
act att tca gcg gtt ttg gct tca gct tgt atg atg gct ctg tgt ttc	14050
Thr Ile Ser Ala Val Leu Ala Ser Ala Cys Met Met Ala Leu Cys Phe	
525 530 535	
caa cag tgc gga tgg cta tcc cat gat ttt ctc cac aat cag gtg ttt	14098
Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His Asn Gln Val Phe	
540 545 550	
gag aca cgc tgg ctt aat gaa gtt gtc ggg tat gtg atc ggc aac gcc	14146
Glu Thr Arg Trp Leu Asn Glu Val Val Gly Tyr Val Ile Gly Asn Ala	
555 560 565	
gtt ctg ggg ttt agt aca ggg tgg tgg aag gag aag cat aac ctt cat	14194
Val Leu Gly Phe Ser Thr Gly Trp Trp Lys Glu Lys His Asn Leu His	
570 575 580 585	
cat gct gct cca aat gaa tgc gat cag act tac caa cca att gat gaa	14242
His Ala Ala Pro Asn Glu Cys Asp Gln Thr Tyr Gln Pro Ile Asp Glu	
590 595 600	
gat att gat act ctc ccc ctc att gcc tgg agc aag gac ata ctg gcc	14290
Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp Ser Lys Asp Ile Leu Ala	
605 610 615	
aca gtt gag aat aag aca ttc ttg cga atc ctc caa tac cag cat ctg	14338
Thr Val Glu Asn Lys Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu	
620 625 630	
ttc ttc atg ggt ctg tta ttt ttc gcc cgt ggt agt tgg ctc ttt tgg	14386
Phe Phe Met Gly Leu Leu Phe Phe Ala Arg Gly Ser Trp Leu Phe Trp	
635 640 645	
agc tgg aga tat acc tct aca gca gtg ctc tca cct gtc gac agg ttg	14434
Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu	
650 655 660 665	

ttg gag aag gga act gtt ctg ttt cac tac ttt tgg ttc gtc ggg aca	14482
Leu Glu Lys Gly Thr Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr	
670 675 680	
gcg tgc tat ctt ctc cct ggt tgg aag cca tta gta tgg atg gcg gtg	14530
Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val	
685 690 695	
act gag ctc atg tcc ggc atg ctg ctg ggc ttt gta ttt gta ctt agc	14578
Thr Glu Leu Met Ser Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser	
700 705 710	
cac aat ggg atg gag gtt tat aat tcg tct aaa gaa ttc gtg agt gca	14626
His Asn Gly Met Glu Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala	
715 720 725	
cag atc gta tcc aca cgg gat atc aaa gga aac ata ttc aac gac tgg	14674
Gln Ile Val Ser Thr Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp	
730 735 740 745	
ttc act ggt ggc ctt aac agg caa ata gag cat cat ctt ttc cca aca	14722
Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro Thr	
750 755 760	
atg ccc agg cat aat tta aac aaa ata gca cct aga gtg gag gtg ttc	14770
Met Pro Arg His Asn Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe	
765 770 775	
tgt aag aaa cac ggt ctg gtg tac gaa gac gta tct att gct acc ggc	14818
Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly	
780 785 790	
act tgc aag gtt ttg aaa gca ttg aag gaa gtc gcg gag gct gcg gca	14866
Thr Cys Lys Val Leu Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Ala	
795 800 805	
gag cag cat gct acc acc agt taa gctagcgtaa accctgcttt aatgagatat	14920
Glu Gln His Ala Thr Thr Ser	
810 815	
gcgagacgcc tatgatcgca tgatatttgc tttcaattct gttgtgcacg ttgtaaaaaa	14980
cctgagcatg tgtagctcag atccttaccg ccggtttcgg ttcattctaa tgaatatatc	15040
accggttact atcgtattttt tatgaataat attctccgtt caattttactg attgtccgtc	15100
gagcaaattt acacattgcc actaaacgtc taaacccttg taatttgttt ttgttttact	15160
atgtgtgtta tgtatttgat ttgcgataaa tttttatatt tgggtactaaa tttataaacac	15220
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tatttttgct ttctaaatac atatactaata caactggaaa tgtaaatatt tgctaataatt	15340
tctactatag gagaattaaa gtgagtgaat atgggtaccac aagggttgga gatttaattg	15400
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ggtaccacac	aagatttgag	gtgcatgaac	gtcacgtgga	caaaagggtt	agtaattttt	15520
caagacaaca	atgttaccac	acacaagttt	tgaggtgcat	gcatggatgc	cctgtggaaa	15580
gtttaaaaat	attttgghaaa	tgatttgcat	ggaagccatg	tgtaaaacca	tgacatccac	15640
ttggaggatg	caataatgaa	gaaaactaca	aattttacatg	caactagtta	tgcatgtagt	15700
ctatataatg	aggattttgc	aatactttca	ttcatacaca	ctcactaagt	tttacacgat	15760
tataattttct	tcatagccag	cagatctaaa	atg gct ccg gat gcg gat aag ctt			15814
			Met Ala Pro Asp Ala Asp Lys Leu			
			820		825	
cga caa cgc cag acg act gcg gta gcg aag cac aat gct gct acc ata						15862
Arg Gln Arg Gln Thr Thr Ala Val Ala Lys His Asn Ala Ala Thr Ile						
		830		835	840	
tcg acg cag gaa cgc ctt tgc agt ctg tct tcg ctc aaa ggc gaa gaa						15910
Ser Thr Gln Glu Arg Leu Cys Ser Leu Ser Ser Leu Lys Gly Glu Glu						
		845		850	855	
gtc tgc atc gac gga atc atc tat gac ctc caa tca ttc gat cat ccc						15958
Val Cys Ile Asp Gly Ile Ile Tyr Asp Leu Gln Ser Phe Asp His Pro						
		860		865	870	
ggg ggt gaa acg atc aaa atg ttt ggt ggc aac gat gtc act gta cag						16006
Gly Gly Glu Thr Ile Lys Met Phe Gly Gly Asn Asp Val Thr Val Gln						
		875		880	885	
tac aag atg att cac ccg tac cat acc gag aag cat ttg gaa aag atg						16054
Tyr Lys Met Ile His Pro Tyr His Thr Glu Lys His Leu Glu Lys Met						
		890		895	900	905
aag cgt gtc ggc aag gtg acg gat ttc gtc tgc gag tac aag ttc gat						16102
Lys Arg Val Gly Lys Val Thr Asp Phe Val Cys Glu Tyr Lys Phe Asp						
		910		915	920	
acc gaa ttt gaa cgc gaa atc aaa cga gaa gtc ttc aag att gtg cga						16150
Thr Glu Phe Glu Arg Glu Ile Lys Arg Glu Val Phe Lys Ile Val Arg						
		925		930	935	
cga ggc aag gat ttc ggt act ttg gga tgg ttc ttc cgt gcg ttt tgc						16198
Arg Gly Lys Asp Phe Gly Thr Leu Gly Trp Phe Phe Arg Ala Phe Cys						
		940		945	950	
tac att gcc att ttc ttc tac ctg cag tac cat tgg gtc acc acg gga						16246
Tyr Ile Ala Ile Phe Phe Tyr Leu Gln Tyr His Trp Val Thr Thr Gly						
		955		960	965	
acc tct tgg ctg ctg gcc gtg gcc tac gga atc tcc caa gcg atg att						16294
Thr Ser Trp Leu Leu Ala Val Ala Tyr Gly Ile Ser Gln Ala Met Ile						
		970		975	980	985
ggc atg aat gtc cag cac gat gcc aac cac ggg gcc acc tcc aag cgt						16342
Gly Met Asn Val Gln His Asp Ala Asn His Gly Ala Thr Ser Lys Arg						

990	995	1000	
ccc tgg gtc aac gac atg cta ggc ctc ggt gcg gat ttt att ggt ggt Pro Trp Val Asn Asp Met Leu Gly Leu Gly Ala Asp Phe Ile Gly Gly 1005 1010 1015			16390
tcc aag tgg ctc tgg cag gaa caa cac tgg acc cac cac gct tac acc Ser Lys Trp Leu Trp Gln Glu Gln His Trp Thr His His Ala Tyr Thr 1020 1025 1030			16438
aat cac gcc gag atg gat ccc gat agc ttt ggt gcc gaa cca atg ctc Asn His Ala Glu Met Asp Pro Asp Ser Phe Gly Ala Glu Pro Met Leu 1035 1040 1045			16486
cta ttc aac gac tat ccc ttg gat cat ccc gct cgt acc tgg cta cat Leu Phe Asn Asp Tyr Pro Leu Asp His Pro Ala Arg Thr Trp Leu His 1050 1055 1060 1065			16534
cgc ttt caa gca ttc ttt tac atg ccc gtc ttg gct gga tac tgg ttg Arg Phe Gln Ala Phe Phe Tyr Met Pro Val Leu Ala Gly Tyr Trp Leu 1070 1075 1080			16582
tcc gct gtc ttc aat cca caa att ctt gac ctc cag caa cgc ggc gca Ser Ala Val Phe Asn Pro Gln Ile Leu Asp Leu Gln Gln Arg Gly Ala 1085 1090 1095			16630
ctt tcc gtc ggt atc cgt ctc gac aac gct ttc att cac tcg cga cgc Leu Ser Val Gly Ile Arg Leu Asp Asn Ala Phe Ile His Ser Arg Arg 1100 1105 1110			16678
aag tat gcg gtt ttc tgg cgg gct gtg tac att gcg gtg aac gtg att Lys Tyr Ala Val Phe Trp Arg Ala Val Tyr Ile Ala Val Asn Val Ile 1115 1120 1125			16726
gct ccg ttt tac aca aac tcc ggc ctc gaa tgg tcc tgg cgt gtc ttt Ala Pro Phe Tyr Thr Asn Ser Gly Leu Glu Trp Ser Trp Arg Val Phe 1130 1135 1140 1145			16774
gga aac atc atg ctc atg ggt gtg gcg gaa tcg ctc gcg ctg gcg gtc Gly Asn Ile Met Leu Met Gly Val Ala Glu Ser Leu Ala Leu Ala Val 1150 1155 1160			16822
ctg ttt tcg ttg tcg cac aat ttc gaa tcc gcg gat cgc gat ccg acc Leu Phe Ser Leu Ser His Asn Phe Glu Ser Ala Asp Arg Asp Pro Thr 1165 1170 1175			16870
gcc cca ctg aaa aag acg gga gaa cca gtc gac tgg ttc aag aca cag Ala Pro Leu Lys Lys Thr Gly Glu Pro Val Asp Trp Phe Lys Thr Gln 1180 1185 1190			16918
gtc gaa act tcc tgc act tac ggt gga ttc ctt tcc ggt tgc ttc acg Val Glu Thr Ser Cys Thr Tyr Gly Gly Phe Leu Ser Gly Cys Phe Thr 1195 1200 1205			16966
gga ggt ctc aac ttt cag gtt gaa cac cac ttg ttc cca cgc atg agc Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro Arg Met Ser 1210 1215 1220 1225			17014

agc gct tgg tat ccc tac att gcc ccc aag gtc cgc gaa att tgc gcc 17062
 Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Lys Val Arg Glu Ile Cys Ala
 1230 1235 1240

aaa cac ggc gtc cac tac gcc tac tac ccg tgg atc cac caa aac ttt 17110
 Lys His Gly Val His Tyr Ala Tyr Tyr Pro Trp Ile His Gln Asn Phe
 1245 1250 1255

ctc tcc acc gtc cgc tac atg cac gcg gcc ggg acc ggt gcc aac tgg 17158
 Leu Ser Thr Val Arg Tyr Met His Ala Ala Gly Thr Gly Ala Asn Trp
 1260 1265 1270

cgc cag atg gcc aga gaa aat ccc ttg acc gga cgg gcg taa 17200
 Arg Gln Met Ala Arg Glu Asn Pro Leu Thr Gly Arg Ala
 1275 1280 1285

agatctgccg gcatcgatcc cgggccatgg cctgctttaa tgagatatgc gagacgccta 17260

tgatcgcatg atatttgctt tcaattctgt tgtgcacgtt gtaaaaaacc tgagcatgtg 17320

tagctcagat ccttaccgcc gggttcgggtt cattctaattg aatatatcac ccgttactat 17380

cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgagctcggc 17440

gcgcctctag aggatcgatg aattcagatc ggctgagtggt ctccttcaac gttgcgggttc 17500

tgtcagttcc aaacgtaaaa cggcttggtc cgcgtcatcg gcgggggtca taacgtgact 17560

cccttaattc tccgctcatg atcagattgt cgtttccgc cttcagttta aactatcagt 17620

gtttgacagg atatattggc gggtaaacct aagagaaaag agcgtttatt agaataatcg 17680

gatatttaaa agggcgtgaa aagggttatc cttcgtccat ttgtatgtgc atgccaacca 17740

cagggttccc ca 17752

<210> 47

<211> 290

<212> PRT

<213> Unknown

<400> 47

Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
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Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
 20 25 30

Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
 35 40 45

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
 50 55 60

Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu

65	70	75	80
Leu Gln Ala	Leu Val	Leu Val His Asn	Leu Phe Cys Phe Ala Leu Ser
	85	90	95
Leu Tyr Met	Cys Val Gly Ile	Ala Tyr Gln Ala Ile Thr	Trp Arg Tyr
	100	105	110
Ser Leu Trp	Gly Asn Ala Tyr	Asn Pro Lys His Lys	Glu Met Ala Ile
	115	120	125
Leu Val Tyr	Leu Phe Tyr	Met Ser Lys Tyr	Val Glu Phe Met Asp Thr
	130	135	140
Val Ile Met	Ile Leu Lys Arg	Ser Thr Arg	Gln Ile Ser Phe Leu His
	145	150	155
Val Tyr His	His Ser Ser Ile	Ser Leu Ile Trp Trp	Ala Ile Ala His
	165	170	175
His Ala Pro	Gly Gly Glu Ala Tyr	Trp Ser Ala Ala	Leu Asn Ser Gly
	180	185	190
Val His Val	Leu Met Tyr Ala Tyr	Tyr Phe Leu Ala	Ala Cys Leu Arg
	195	200	205
Ser Ser Pro	Lys Leu Lys Asn Lys Tyr	Leu Phe Trp Gly	Arg Tyr Leu
	210	215	220
Thr Gln Phe	Gln Met Phe Gln Phe Met	Leu Asn Leu Val	Gln Ala Tyr
	225	230	235
Tyr Asp Met	Lys Thr Asn Ala Pro Tyr	Pro Gln Trp Leu Ile	Lys Ile
	245	250	255
Leu Phe Tyr	Tyr Met Ile Ser Leu	Leu Phe Leu Phe Gly	Asn Phe Tyr
	260	265	270
Val Gln Lys	Tyr Ile Lys Pro Ser Asp	Gly Lys Gln Lys Gly	Ala Lys
	275	280	285
Thr Glu			
	290		

<210> 48
 <211> 525
 <212> PRT
 <213> Unknown

<400> 48
 Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
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 20 25 30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
 35 40 45
 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
 50 55 60
 Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
 65 70 75 80
 Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
 85 90 95
 Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
 100 105 110
 His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
 115 120 125
 Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
 130 135 140
 Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
 145 150 155 160
 Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
 165 170 175
 Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
 180 185 190
 Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
 195 200 205
 Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
 210 215 220
 Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
 225 230 235 240
 Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
 245 250 255
 Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
 260 265 270
 Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
 275 280 285
 Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
 290 295 300
 Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
 305 310 315 320
 Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
 325 330 335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
 340 345 350
 Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
 355 360 365
 Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
 370 375 380
 Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
 385 390 395 400
 Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
 405 410 415
 Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
 420 425 430
 Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
 435 440 445
 Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
 450 455 460
 His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
 465 470 475 480
 Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
 485 490 495
 Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu
 500 505 510
 Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser
 515 520 525

<210> 49
 <211> 469
 <212> PRT
 <213> Unknown

<400> 49

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
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 Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
 20 25 30
 Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
 35 40 45
 Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
 50 55 60
 Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
 65 70 75 80

Thr	Glu	Lys	His	Leu	Glu	Lys	Met	Lys	Arg	Val	Gly	Lys	Val	Thr	Asp	85	90	95	
Phe	Val	Cys	Glu	Tyr	Lys	Phe	Asp	Thr	Glu	Phe	Glu	Arg	Glu	Ile	Lys	100	105	110	
Arg	Glu	Val	Phe	Lys	Ile	Val	Arg	Arg	Gly	Lys	Asp	Phe	Gly	Thr	Leu	115	120	125	
Gly	Trp	Phe	Phe	Arg	Ala	Phe	Cys	Tyr	Ile	Ala	Ile	Phe	Phe	Tyr	Leu	130	135	140	
Gln	Tyr	His	Trp	Val	Thr	Thr	Gly	Thr	Ser	Trp	Leu	Leu	Ala	Val	Ala	145	150	155	160
Tyr	Gly	Ile	Ser	Gln	Ala	Met	Ile	Gly	Met	Asn	Val	Gln	His	Asp	Ala	165	170	175	
Asn	His	Gly	Ala	Thr	Ser	Lys	Arg	Pro	Trp	Val	Asn	Asp	Met	Leu	Gly	180	185	190	
Leu	Gly	Ala	Asp	Phe	Ile	Gly	Gly	Ser	Lys	Trp	Leu	Trp	Gln	Glu	Gln	195	200	205	
His	Trp	Thr	His	His	Ala	Tyr	Thr	Asn	His	Ala	Glu	Met	Asp	Pro	Asp	210	215	220	
Ser	Phe	Gly	Ala	Glu	Pro	Met	Leu	Leu	Phe	Asn	Asp	Tyr	Pro	Leu	Asp	225	230	235	240
His	Pro	Ala	Arg	Thr	Trp	Leu	His	Arg	Phe	Gln	Ala	Phe	Phe	Tyr	Met	245	250	255	
Pro	Val	Leu	Ala	Gly	Tyr	Trp	Leu	Ser	Ala	Val	Phe	Asn	Pro	Gln	Ile	260	265	270	
Leu	Asp	Leu	Gln	Gln	Arg	Gly	Ala	Leu	Ser	Val	Gly	Ile	Arg	Leu	Asp	275	280	285	
Asn	Ala	Phe	Ile	His	Ser	Arg	Arg	Lys	Tyr	Ala	Val	Phe	Trp	Arg	Ala	290	295	300	
Val	Tyr	Ile	Ala	Val	Asn	Val	Ile	Ala	Pro	Phe	Tyr	Thr	Asn	Ser	Gly	305	310	315	320
Leu	Glu	Trp	Ser	Trp	Arg	Val	Phe	Gly	Asn	Ile	Met	Leu	Met	Gly	Val	325	330	335	
Ala	Glu	Ser	Leu	Ala	Leu	Ala	Val	Leu	Phe	Ser	Leu	Ser	His	Asn	Phe	340	345	350	
Glu	Ser	Ala	Asp	Arg	Asp	Pro	Thr	Ala	Pro	Leu	Lys	Lys	Thr	Gly	Glu	355	360	365	
Pro	Val	Asp	Trp	Phe	Lys	Thr	Gln	Val	Glu	Thr	Ser	Cys	Thr	Tyr	Gly	370	375	380	

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
 385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
 405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
 420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
 435 440 445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
 450 455 460

Leu Thr Gly Arg Ala
 465

<210> 50
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Polylinker

<400> 50
 gaattcggcg cgccgagctc ctcgag 26

<210> 51
 <211> 265
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Polylinker-terminator-polylinker

<400> 51
 ccaccgcggt gggcggccgc ctgcagtcta gaaggcctcc tgctttaatg agatatgcga 60
 gacgcctatg atcgcatgat atttgctttc aattctgttg tgcacgttgt aaaaaacctg 120
 agcatgtgta gctcagatcc ttaccgccgg ttccggttca ttctaataa tatatcaccc 180
 gttactatcg tatttttatg aataatattc tccgttcaat ttactgattg tccgtcgacg 240
 aattcgagct cggcgcgcca agctt 265

<210> 52
 <211> 257
 <212> DNA
 <213> Artificial sequence

<220>

<223> Polylinker-terminator-polylinker

<400> 52

ggatccgata tcgggccgcg tagcgttaac cctgctttaa tgagatatgc gagacgccta 60
tgatcgcgatg atatttgctt tcaattctgt tgtgcacggt gtaaaaaacc tgagcatgtg 120
tagctcagat ccttaccgcc ggtttcgggt cattctaata aatatatcac ccgttactat 180
cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgaattcgag 240
ctcggcgcgc caagctt 257

<210> 53

<211> 257

<212> DNA

<213> Artificial sequence

<220>

<223> Polylinker-terminator-polylinker

<400> 53

agatctgccg gcatcgatcc cgggccatgg cctgctttaa tgagatatgc gagacgccta 60
tgatcgcgatg atatttgctt tcaattctgt tgtgcacggt gtaaaaaacc tgagcatgtg 120
tagctcagat ccttaccgcc ggtttcgggt cattctaata aatatatcac ccgttactat 180
cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgaattcgag 240
ctcggcgcgc caagctt 257

□